

A.

**HPIV3 L aa 456 (RSV L aa 521) F→L**  
AEISYEYTLKHWKEISLIEFRKCFDFDPGEELSIFMKDKA-HPIV2 F460  
SAISYENAVDYYQSFIGIKFNKFIEPQLDEDLTIYMKDKA-HPIV3  
SAISYECAVDNYSSFIGFKFLKFIEPQLDEDLTIYMKDKA-HPIV1

B.

**HPIV3 cp45 L aa 942 Y→H**  
LLPSQLGGLNYLACSLFNRN-HPIV2 Y948  
LIPASVGGFNYMAMSRCFVRN-HPIV3  
LIPANIGGFNYMSTARCFVRN-HPIV1

C.

**HPIV3 cp45 L aa 992 L→F**  
LARKPGKGSWATLAADPYSLN-HPIV2 A998  
MNQE\_PGESSFLDWASDPYSCN-HPIV3  
MNQE\_PGDSSFLDWASDPYSCN-HPIV1

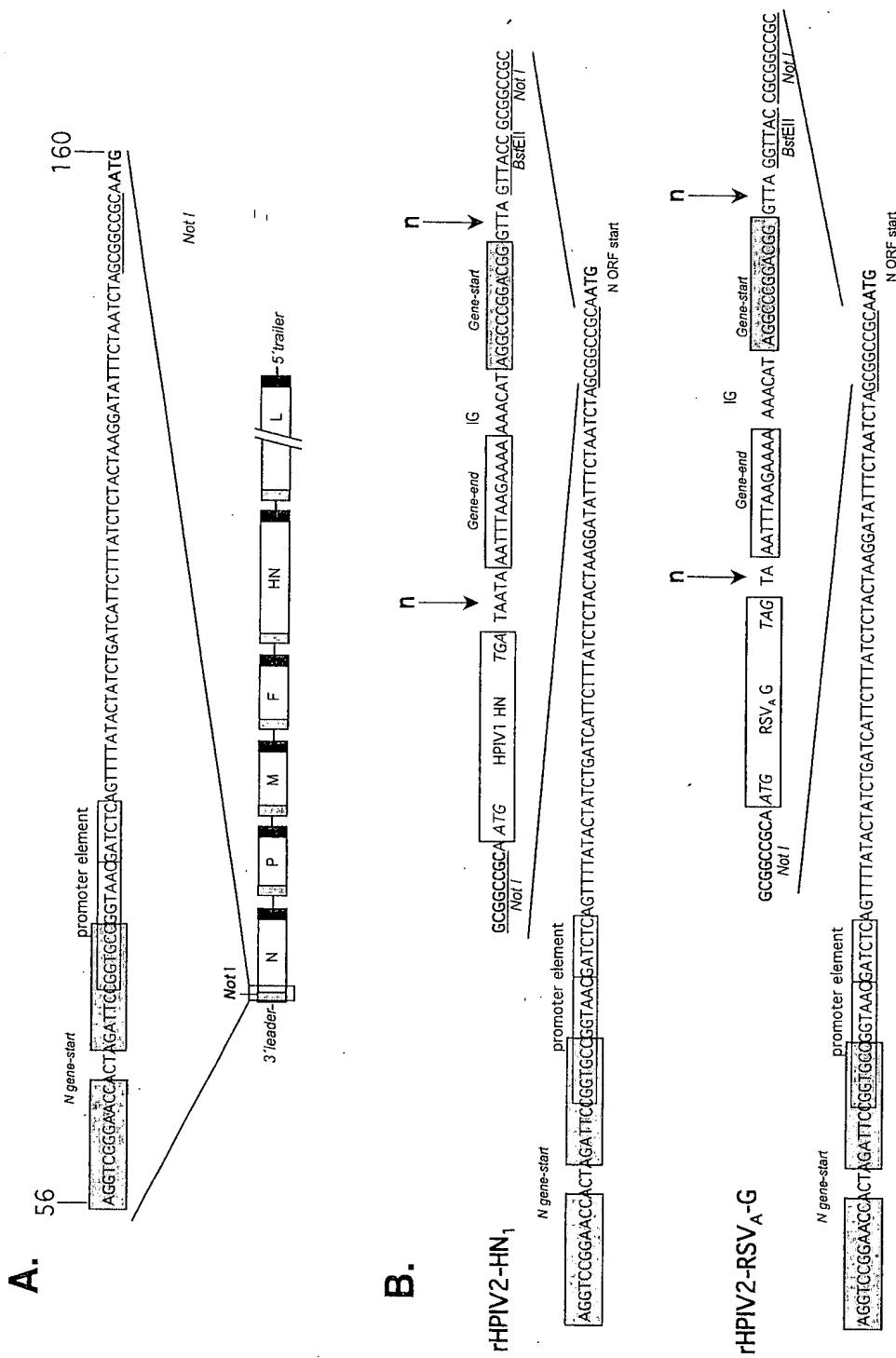
D.

**HPIV3 cp45 L aa 1558 T→I**  
DIITPIHAPYLASLDYVKLSI-HPIV2 L1566  
GVLNPIYGPNTASQDQIKLAL-HPIV3  
GVVEPVYGPNLNSNQDKILLAI-HPIV1

E.

**BPIV3 L aa 1711 T→I**  
EQLETDIILHSTLTA-HPIV2 S1724  
EDNILDNIVKTVNDN-BPIV3  
EDNMLDNIVKTVNDN-HPIV3  
ADSMLDNITAEVQHN-HPIV1

**FIGURE 1**



**FIGURE 2**

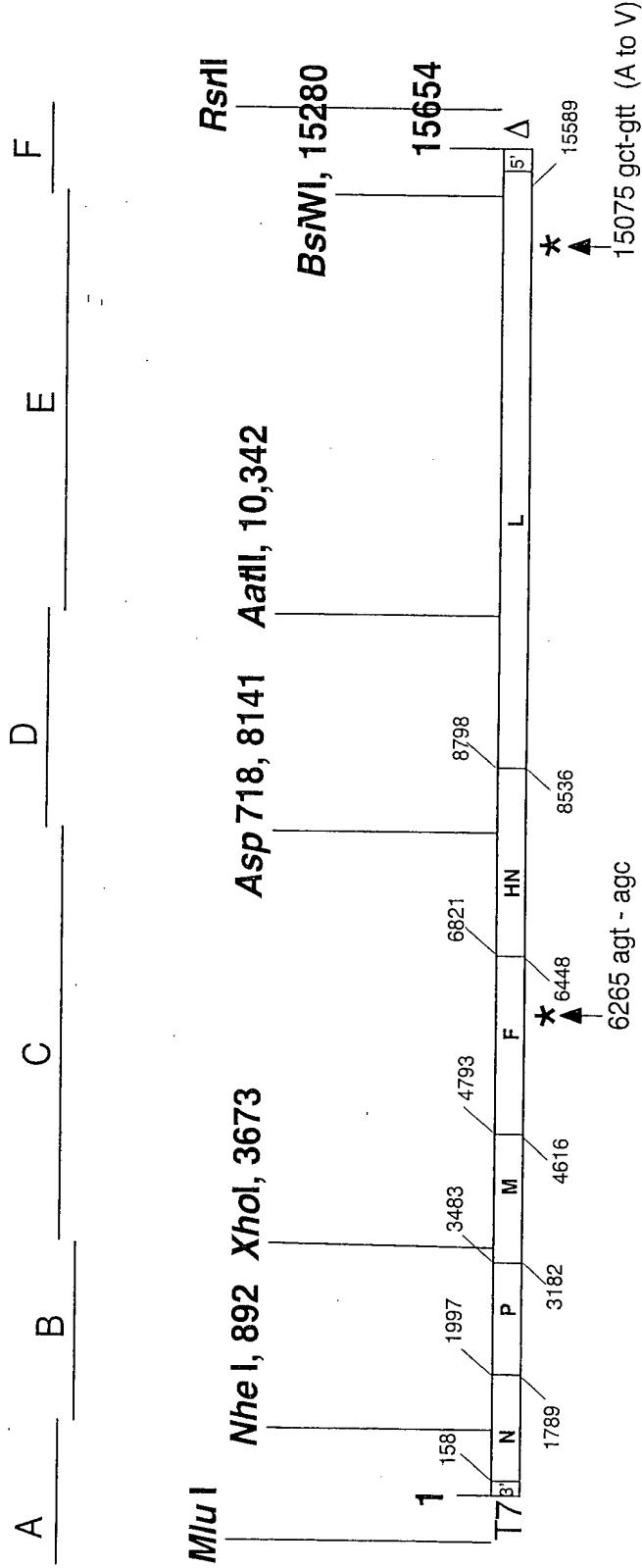
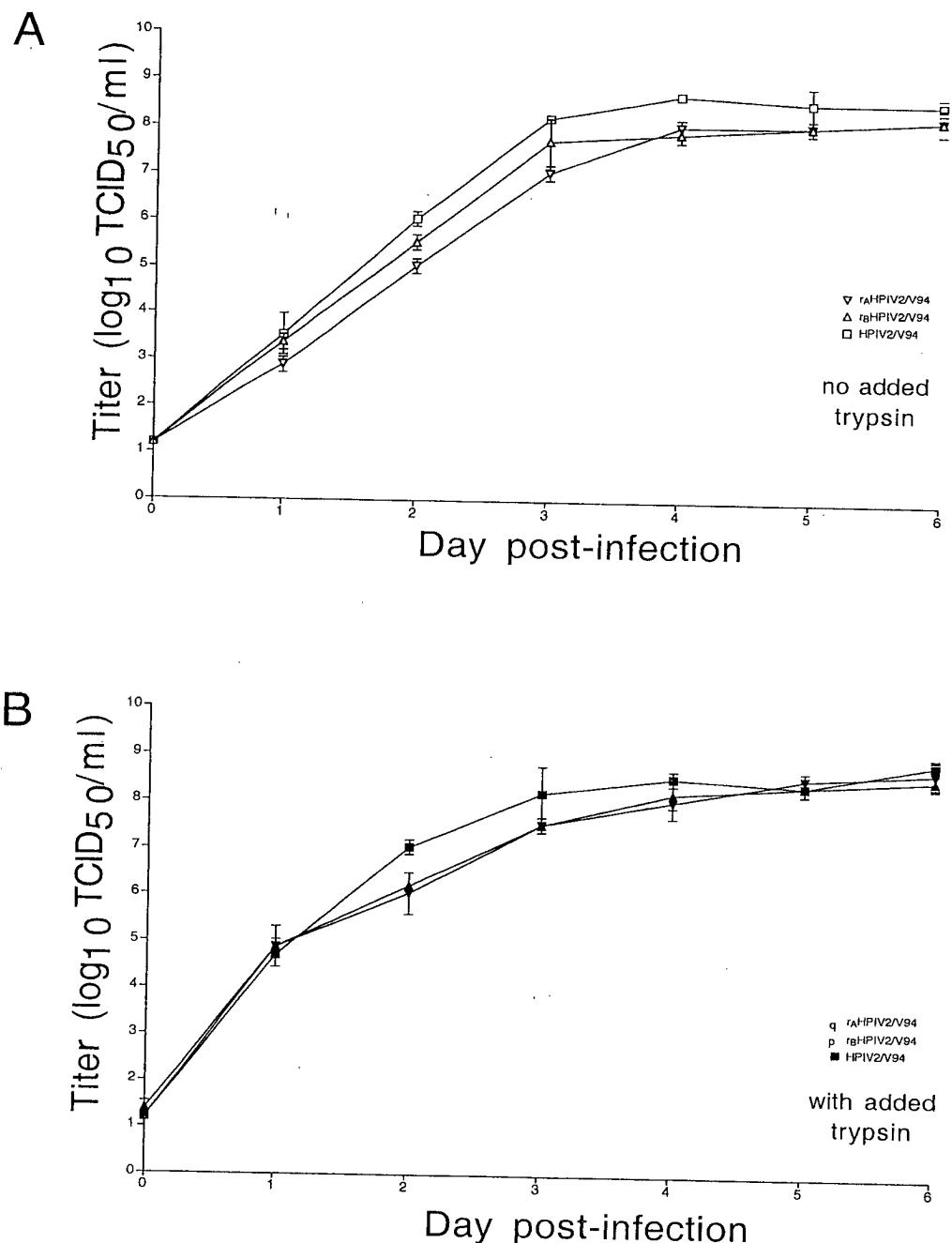
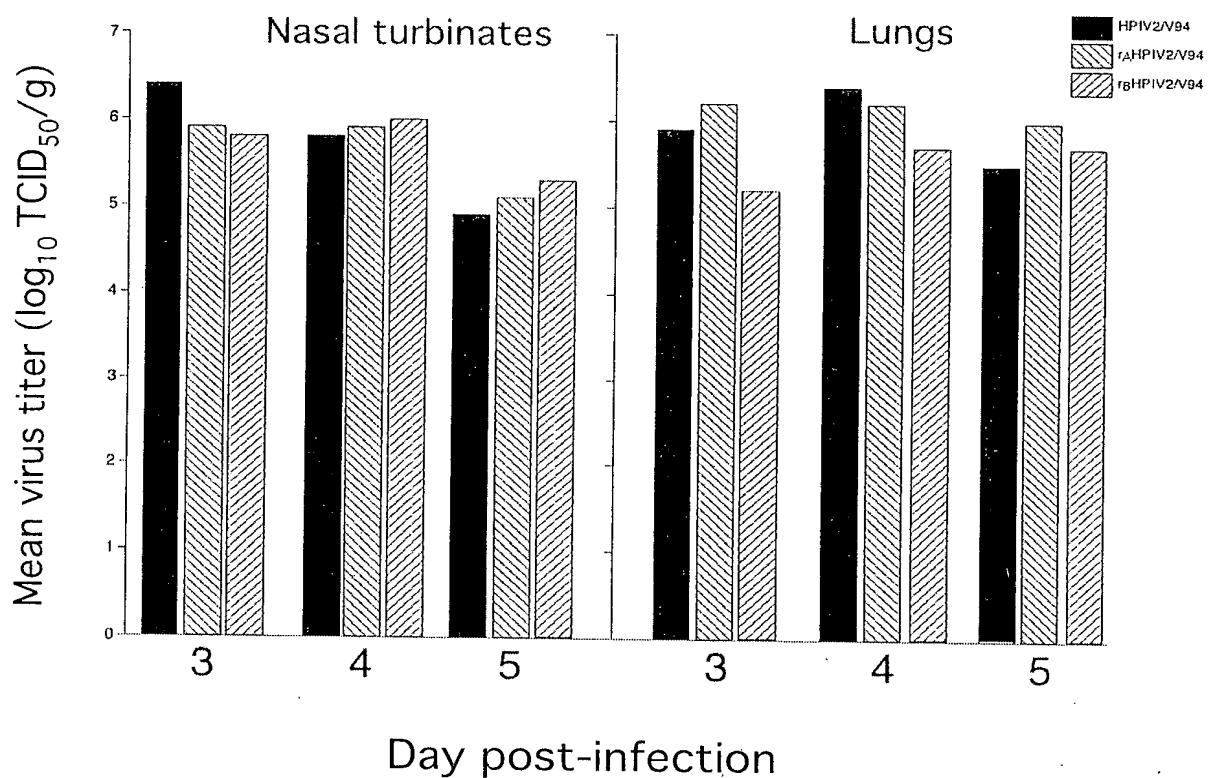


FIGURE 3



**FIGURE 4**



**FIGURE 5**

**A**

51	TACGTAGTCCCGAACCACTAGATT . CGGTGCCGGTAACGATTCCAGTTT	99	Toshiba
51	TACGTAGTCCCGAACCACTAGATTCCGGTGCCGGTAACGATTCCAGTTT	100	Greer

**B**

700	ATGACTGCTCCTGATCAACCACCAGTATCAGTAGCAA...GATGGCTAA	746	Toshiba
701	ATGACTGCTCCTGATCAACCACCAGTATCAGTAGCAAAGCGGATGGCTAA	750	Greer

**C**

1897	TCTCTCATATAATTAAAGAAAAAATCATAGG . CCGGACGGGTTAGAAATCC	1945	Toshiba
1901	TCTCTCATATAATTAAAGAAAAAATCATAGGCCGGACGGGTTAGAAATCC	1949	Greer

**D**

2896	AGTAATTGCCGGTCCA ACTAGTGGAGGCTTCACAGCCGAA . CAGGTGATA	2944	Toshiba
2900	AGTAATTGCCGGTCCA ACTAGTGGAGGCTTCACAGCCGAAGGCAGTGATA	2949	Greer

**E**

2945	TTGATTTCAATGGATGA ACTAGCTAGACCTACACTCTCATCAACAAAAAG	2994	Toshiba
2950	.TGATTTCAATGGATGA ACTAGCTAGACCTACACTCTCATCAACAAAAAG	2998	Greer

**F**

8595	TTATACGTTTGGCTGTATTAGAATGTTATAG . ATTCTGCTGTTTCCC	8643	Toshiba
8599	TTATACGTTTGGCTGTATTAGAATGTTATAGCATTCTGCTGTTTCCC	8648	Greer

**G**

9894	TGGGGTCATCCCACTCTACTGCTGCGCAA...GTGGGTAAAGTGAGAGA	9940	Toshiba
9899	TGGGGTCATCCCACTCTACTGCTGCGCAAGCTGCAGGTAAAGTGAGAGA	9948	Greer

**H**

10991	TGATATCTTATAGTCT . . . CCAAGGGAGGTATTGAAGGCCTATGTCAGA	11037	Toshiba
10999	TGATATCTTATAGTCTCTCCAAAGGGAGGTATTGAAGGCCTATGTCAGA	11048	Greer

**I**

13938	ACAGATATAATTCTTCACTCTACTTTAACTGCTCCTTATGATAATTAGA	13987	Toshiba
13949	ACAGATATAATTCTTCACTCTACTTTAACTGCTCCTTATGATAATTAGA.	13997	Greer

**J**

13988	AAACTCTAACAAAGTTGATTATCCCTTTCGACATTTCCACATCCAG	14037	Toshiba
13998	AAACTCTAACAAAGTTGATTATCCCTT..GACATTTCCACATCCAG	14045	Greer

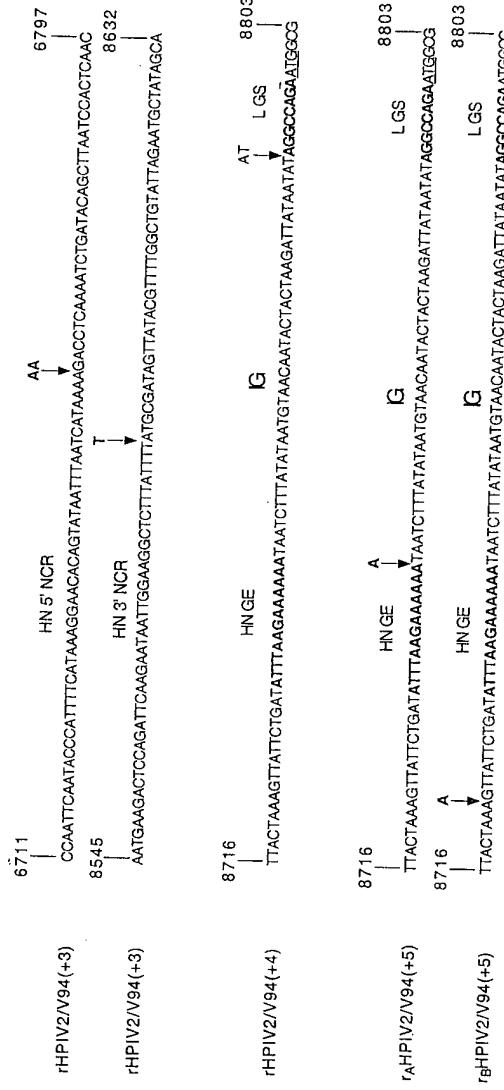
A. Site of insertion of oligonucleotides at an *EcoRV* restriction site in the L polymerase coding sequence

HPIV2 nt 15554↑  
GAT ATC GAG AGG GGT ATC GAT GGC GAA GAA TTA **TGA** CAA CAG TGA  
 end of L coding region ↑

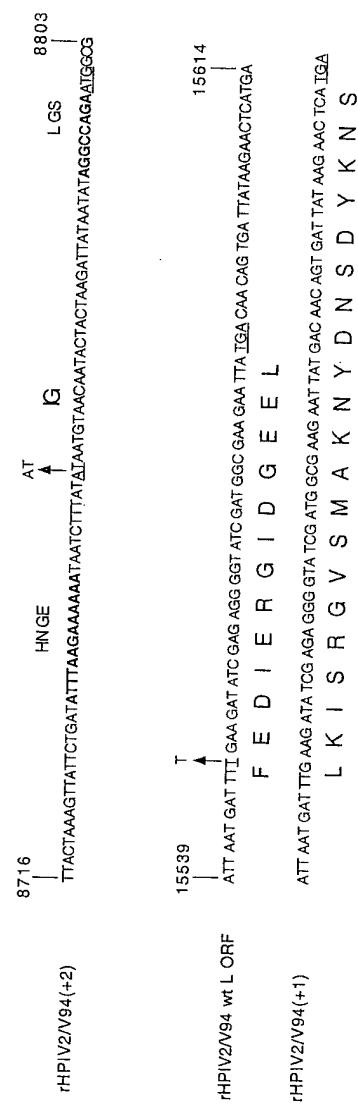
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Designation of recovered virus	Oligonucleotide inserted into EcoRV site:	Size of insert	(polyhexameric length; length of cDNA)
rHPV2/V94 (+6)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGA	+42 nts	(6n ; 15696 nts)
rHPV2/V94 (+1)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGA	+43 nts	(6n + 1; 15697 nts)
rHPV2/V94 (+2)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGA	+44 nts	(6n + 2; 15698 nts)
rHPV2/V94 (+3)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGA	+45 nts	(6n + 3; 15699 nts)
rHPV2/V94 (+4)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGAAC	+46 nts	(6n + 4; 15700 nts)
rHPV2/V94 (+5)	<u>AT</u> TGAGAGGGTATCGATGGCAGAATT <u>TG</u> ACAACAGTGAAC	+47 nts	(6n + 5; 15701 nts)

## A Genome length modified by nt insertion



## B Genome length modified by nt deletion



Docket No.: 2303-44-3  
 Inventors: Skiadopoulos et al  
 Title: Recovery of Recombinant Human  
 Parainfluenza Virus Type 2 . . .  
 Attorney: Jeffrey J. King (425.455-5575)  
 Sheet 8 of 29

FIGURE 8

Human Parainfluenza Virus Type 2 Strain V94 antigenomic sense cDNA Sequence Range: 1 to 15654

10	20	30	40	50	60	70	80	90	100
ACCAAGGGGA	GAATCAGATG	GCATCGTTAT	ATGACGAATT	GCAAAAGAT	TACGTAGGTC	CGGAACCCT	AGATTCCGGT	GCCGGTAACG	ATCTCAGTT
110	120	130	140	150	160	170	180	190	200
TATACTATCT	GATCATTCTT	TATCTCTACT	AAGGATATTT	CTAATCTAAG	GTTCAAATG	TCAAGTGCT	TAAAGACATT	TGAAAGATT	ACTATACAAAC
210	220	230	240	250	260	270	280	290	300
AGGAGCTTCA	GGAGCAATCT	GAAGACACTC	CAATACCTCT	TGAAAACAATC	AGACCTACAA	TCAGAGTATT	TGTCATCAAT	AATAATGATC	CTATTGTAAG
310	320	330	340	350	360	370	380	390	400
ATCTAGACTT	TTATTCTTTA	ATCTACGAAT	TATTATGAGT	AACACTGCAA	GAGAGGGACA	TAGAGCTGGT	GCTCTCCTCA	GTCTTTTATC	ACTACCTCT
410	420	430	440	450	460	470	480	490	500
GCAGCTATGA	GTAATCACAT	CAAACATGCC	ATGCATTCA	CAGAACCCAG	CATAGATAGA	GTAGAAATAA	CAGGGTTGTA	GAATAATTCA	TTCCGAGTTA
510	520	530	540	550	560	570	580	590	600
TTCCAGATGC	TCGATCAACT	ATGTCAGAG	GAGAAAGTGC	GGCCTTCGAA	GCATTAGCTG	AGGACATTCC	TGATACCCCT	AATCACCAAA	CTCCATTGTT
610	620	630	640	650	660	670	680	690	700
AAATAATGAT	GTGGAAGATG	ACATATTTGA	TGAAACAGAG	AAATTCTTGG	ATGTTGCTA	TAGTGTACTT	ATGCAGGCAT	GGATAGTAAC	ATGCAAGTGC
710	720	730	740	750	760	770	780	790	800
ATGACTGCTC	CTGATCAACC	ACCAGTATCA	GTAGCAAAGC	GGATGGCTAA	ATATCAACAA	CAAGGGAGAA	TCAATGCTAG	ATATGTACTA	CAACCTGAAG
810	820	830	840	850	860	870	880	890	900
CACAAAGACT	AATTCAAAAT	GCCATCCGCA	AGTCATGGT	AGTAAGGCAT	TTCATGACCT	ATGAGCTTCA	ACTTCACAA	TCAAGATCTT	TGCTAGCGAA
910	920	930	940	950	960	970	980	990	1000
CCGTTATTAT	GCCATGGTGG	GAGACATTGG	CAAGTATATT	GAACACAGCG	GAATGGGAGG	GTTCCTTCTTA	ACACTTAAAT	ATGGACTTGG	AACAAGATGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
CCTACATTGG	CTCTTGCGAC	ATTCTCTGGG	GAACCTCAGA	AATTAAAGGC	TCTCATGCTA	CATTATCAGA	GTCTAGGACC	CATGCCAAG	TACATGGCTC
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TATTAGAATC	ACCAAAGCTG	ATGGATTTTG	TCCCCTCTGA	ATATCCATTA	GTTTATAGT	ATGCAATGGG	TATTGGAACT	GTCTTGATA	CAAACATGAG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AAACTATGCA	TATGGTAGAT	CATATCTAAA	TCCACAAATAT	TTTCAGCTAG	GGGTAGAAC	AGCAAGGAAA	CAGCAAGGAG	CTGTTGACAA	CAGGACAGCA
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
GAGGACCTCG	GCATGACTGC	TGCAAGATAAA	GCAGACCTCA	CTGCAACCAT	ATCAAAGCTA	TCTTTATCCC	AATTACCTAG	GGGTAGACAA	CCAATATCCG
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ACCCATTGTC	TGGAGCAAAT	GACAGAGAAA	CAGGAGGACA	AGCAACTGAT	ACACCTGTGT	ATAACCTCAA	TCCAATCAAT	AATCGGAGGT	ATGACAACTA
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
TGACAGTGT	AGTGAGGACA	GAATTGACAA	CGATCAAGAT	CAGGCTATCA	GAGAGAACAG	AGGAGAACCT	GGACAACCAA	ACAACCAGAC	AAGCGAAAC
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
CAGCAGAGAC	TCAATCTCCC	TGTACCGCAA	AGAACATCAG	GTATGAGTAG	TGAAGAGTTC	CAACATTCAA	TGAATCAGTA	CATCCGTGCT	ATGCATGAGC
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
AATAACAGAG	CTCCCCAGGT	GATGATGCCA	ATGATGCCA	AGATGGGAAT	GACATTTCAC	TTGAGCTAGT	TGGAGATTTT	GATTCCAAAC	TCTCACTTTC
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
ACATAACCAAG	ACATACACAT	CCACACCC	CAGAGACATA	GCTACCCAC	ACACACTCAC	CCAGACAAAT	CAAACATAGAT	TCAAATCATT	CGGAAACAAAT
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
TCTCCTGAA	TTTAAGAAAA	AAACATAGGC	CCGGACGGGT	TAGAGATCGG	GTGCTGTC	GTGCCAGAC	AACCTCCACA	CCAGAGCCAC	ACAATCATGG
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
CCGAGGAAC	AAACATACACC	ACTGAGCAAG	TTGATGAATT	AATCCATGCT	GGACTAGGAA	CAGTAGATTT	CTTCCTATCT	AGACCCATAG	ATGCTCAGTC
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TTCTTTAGGT	AAAGGCAGCA	TCCCACCAAG	TGTACGGCT	GTTCTAACTA	ATGCAAGCAGA	GGCAAAATCC	AAACCAAGTTG	CTGCTGGTCC	AGTAAAACCC
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
AGACGGAGA	AAAGTGTACAG	CAATACCACT	CCATACACTA	TTGCAAGACAA	CATCCACCT	GAGAAGCTAC	CGATCAACAC	TCCAATACCC	AATCCATTAC
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
TTCCACTGGC	ACGCCCTCAC	GGAAAGATGA	CAGACATTGA	CATTGTCACT	GGGAACATTA	CAGAAGGATC	ATACAAAGGT	GTGGAGCTTG	CCAAATTAGG
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
GAAGCAAACA	CTACTCACAA	GGTTCACCTC	GAATGAGCCA	GTCTCCTCAG	CTGGATCCGC	CCAAGACCCC	AACTTTAAGA	GGGGGGGAGC	TAATAGAGAA
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
AGAGCAAAGAG	GCAACCATAG	GAGAGAATGG	AGTATTGCT	GGGTCGGAGA	TCAGGTCAA	GTCTTCGAGT	GGTGTAAATCC	CAGGTGTGCC	CCAGTCACGG
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
CTTCAGCTCG	CAAGTTCAC	TGCAACATGTG	GATCCTGCC	CAGCATCTGC	GGAGAATCTG	AAGGAGATCA	TTGAGCTCTT	AAAAGGGCTT	GATCTTCGCC
2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
TTCAGACTGT	AGAAGGGAAA	GTAGATAAAA	TTCTTGCAAC	CTCTGCAACT	ATAATCAATC	TTAAAAATGA	AATGACTAGT	CTTAAGGCAGA	GCGTTGCAAC
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
TGTGGAAGGT	ATGATAACAA	CAATTAAAT	CATGGATCCC	AGTACACCAA	CCAATGTC	TGAGAGGAG	ATCAGAAAGA	GTTCACACAA	TGTTCCAGTA

FIGURE 9A

2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
GTAATTGCTG	GTCCGACTAG	TGGAGGCCTTC	ACAGCGGAAG	GCAGTGACAT	GATTTCAATG	GATGAACTAG	CTAGGCCCTAC	ACTCTCATCA	ACAAAAAAGA
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
TCACACGAAA	GCCTGAATCC	AAGAAAGATT	TAACAGGCAT	AAAACTAACC	CTGATGCAGC	TTGCAAATGA	CTGCATCTCG	CGTCCAGATA	CCAAGACTGA
3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
-GTTTGTGACT	AAGATTCAAG	CAGCAACCAC	AGAACATCACAG	CTCAACGAAA	TCAAACGGTC	AATAATACGC	TCTGCAATAT	AAAATGCGGT	GCAATCACAC
3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
AAGAGACATT	CAACATGCAT	CCGATCAAGA	TCCAAACTCC	TTCCATCCGA	AAACACACTC	ACCACTGTCA	ACACCAAGAA	ACAACATACAG	CCGAACCATG
3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
CTCAACAAA	AGACCCAAAC	AACATCTCAA	ATCGACAGAA	GGCTAGACAT	GATAAAATTAA	ATAAAAAAATT	AAAAGAAGTT	AAGTAAAATT	TAAAGAACAC
3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
AATAGAGAAA	ACCTAGGTCC	GAAAGCTTGC	CTTTCAGACAA	GATCCCCAAA	TCATAGTTCA	AACTTCAAAC	ACAGCAGCAG	ACATGCCAT	AATATCATTA
3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
CCAGCAGATC	CAACTTCACC	CAGTCATC	CTTACTCGCT	TTCCAATACAA	ACTTGATACC	AAAGATGGCA	AGGCAGGGAA	ACTCCTTAA	CAGATTAGAA
3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
TTAGGTATCT	AAATGAACCT	AACTCTCGTC	ATACACCAAAT	AACTTCATC	AATACGTATG	GATTTGTTA	TGCTCGAGAC	ACTTCAGGAG	GCATTCACAG
3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
CGAGATCAGC	AGTGANCCAG	CTGCAGGGTC	CATAACGGCA	TGCATGATGA	CACTAGGTCTC	TGGTCCAAAT	ATTTCAGAATG	CAAATCTAGT	GCTAAGATCC
3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
CTGAATGAAT	TCTACGTAAA	AGTCAAGAAG	ACATCAAGCC	AGAGGGAGGA	AGCAGTGT	GAATTAGTTA	ACATTCCAAAC	CTTATTGAGA	GAACATGCTC
3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
TTGCAAAACG	CAAACACGTTA	GTATGCTCTG	CAGAAAAATT	CCTCAAGAAC	CCATCAAAGC	TACAAGCTGG	ATTGAAATAT	GTATACATCC	CAAACACGTTG
4010	4020	4030	4040	4050	4060	4070	4080	4090	4100
CTCCATTACA	TACTCACCAC	GAAATCTGAA	TTACCAAGTT	GCCAGACCTA	TCCTTAAGTT	CAGATCACGC	TTTGTGTATA	GCATTCAATT	GGAATTAAATC
4110	4120	4130	4140	4150	4160	4170	4180	4190	4200
CTGAGATTCG	TATGCAATC	TGACTCCCCT	TTGATGAAAT	CTTATAATGC	AGATCGAAC	GGTCGAGGAT	GCCTCGCATC	AGTCTGGATC	CACGTATGTA
4210	4220	4230	4240	4250	4260	4270	4280	4290	4300
ACATTCTGAA	AAACAAAAGC	ATCAAGAAC	AAGGCAGAGA	ATCATATTTC	ATAGCTAAGT	GCATGAGTAT	GCAGCTGCAG	GTGTCCATTG	CAGATCTTGC
4310	4320	4330	4340	4350	4360	4370	4380	4390	4400
GGGACCAACA	ATCATAATTAA	AATCATTTGGG	TCACATCCCC	AAAGACTGCAC	TTCTTTTTT	CAGCAAAGAC	GGGATTGCCT	GTCATCCACT	ACAAGATGTT
4410	4420	4430	4440	4450	4460	4470	4480	4490	4500
TCCCCCTACTC	TGACAAAATC	ACTGTGGTCA	GTGGGATGTG	AGATAGAAC	TGCCAAGTTG	ATACTTCAAG	AATCTGATAT	TAATGAGCTA	ATGGGCCACC
4510	4520	4530	4540	4550	4560	4570	4580	4590	4600
AGGACTTGTAT	TACTGATAAG	ATTGCCATTA	GATCAGGTCA	ACGGCATT	GAGAGGTCCA	AATTCAAGCCC	ATTCAAAAAAA	TACGCATCAA	TTCCAAACATT
4610	4620	4630	4640	4650	4660	4670	4680	4690	4700
AGAAGCCATC	AACTGAATGC	TCCAGCATCT	AGGAATAGAA	CAACAACTAA	GTCATACCAT	TATTGACCAT	ACAATAATCA	ACAATTTTAG	CCAACTGATT
4710	4720	4730	4740	4750	4760	4770	4780	4790	4800
ACTAAGATAT	TATCATAGTT	CCGAACTGTAT	CAATCTAACAA	AAAAAAACTAA	ACATTCAATA	ATAAAATCAA	GTTCAGGCCA	AATTATCCAG	CCATGCATCA
4810	4820	4830	4840	4850	4860	4870	4880	4890	4900
CCTGCATCCA	ATGATAGTAT	GCATTTTTGT	TATGTACACT	GGAATTGTAG	GTTCAGATGC	CATTGCTGGA	GATCAACTCC	TCAATGTAGG	GGTCATTCAA
4910	4920	4930	4940	4950	4960	4970	4980	4990	5000
TCAAAGATAA	GATCACTCAT	GTACTACACT	GATGGTGCGC	CTAGCTTAT	TGTTGAAAAA	TTACTACCCA	ATCTTCCCCC	AAGCAATGGA	ACATGCAACA
5010	5020	5030	5040	5050	5060	5070	5080	5090	5100
TCACCACTCT	AGATGCATAT	AATGTTACCC	TATTTAAGTT	GCTAACACCC	CTGATTGAGA	ACCTGAGCAA	AATTCTGCT	GTTACAGATA	CCAAACCCCG
5110	5120	5130	5140	5150	5160	5170	5180	5190	5200
CCGAGAACGA	TTTGAGGAG	TCGTTATTGG	GCTGCTGCA	CTAGGAGTAG	CTACAGCTGC	ACAAATAACCC	GCAGCTGTAG	CAATAGTAAA	AGCCAATGCA
5210	5220	5230	5240	5250	5260	5270	5280	5290	5300
AATGCTGCTG	CGATAAAACAA	TCTTGCATCT	TCAATTCAAT	CCACCAACAA	GGCAGTATCC	GATGTGATAA	CTGCATCAAG	AAACATTGCA	ACCGCAGTTTC
5310	5320	5330	5340	5350	5360	5370	5380	5390	5400
AAGCGATTCA	GGATCACATC	AATGGAGCCA	TTGTCACACGG	GATAACATCT	GCATCATGCC	GTGCCCATGAA	TGCACTAATT	GGGTCAATAT	TAAATTGTA
5410	5420	5430	5440	5450	5460	5470	5480	5490	5500
TCTCACTGAG	CTTACTACAA	TATTCATCAA	TCAAATAACCA	AACCCCTGCGC	TGACACCCT	TTCCATCAA	GCTTTAAGAA	TCCTCCCTCGG	TAGCACCTTG
5510	5520	5530	5540	5550	5560	5570	5580	5590	5600
CCAATTGTC	TTGAATCCAA	ACTCAACACA	AAACTCAACAA	CAGCAGAGCT	GCTCAGTTCC	GGACTGTAA	CTGGTCAAAT	AATTTCATT	TCCCCAATGT
5610	5620	5630	5640	5650	5660	5670	5680	5690	5700
ACATGCAAAT	GCTAATTCAA	ATCAATGTC	CGACATTAT	AATGCAACCC	GGTGCAGAAGG	TAATTGATCT	AATTGCTATC	TCTGCAAACCC	ATAAATTACA
5710	5720	5730	5740	5750	5760	5770	5780	5790	5800
AGAAGTAGTT	GTACAAGTTC	CTAATAGAAAT	TCTAGAAAT	GCAAATGAAC	TACAAAACCA	CCCAGCCAAT	GATTGTCGCG	TGACACCAAA	CTCTGTATTT

FIGURE 9B

5810	5820	5830	5840	5850	5860	5870	5880	5890	5900
TGTAGATACA	ATGAGGGTTC	CCCGATCCCT	GAATCACAAAT	ATCAATGCTT	AAGGGGGAAT	CTTAATTCTT	GCACCTTTAC	CCCTATTATC	GGGAACTTC
5910	5920	5930	5940	5950	5960	5970	5980	5990	6000
TCAAGCGATT	CGCATTTGCC	AATGGTGTGC	TCTATGCCAA	CTGCAAATCT	TTGCTATGTA	AGTGTGCCGA	CCCTCCCCAT	GTTGTGTCTC	AAGATGACAA
6010	6020	6030	6040	6050	6060	6070	6080	6090	6100
CCAAGGCATC	AGCATAATTG	ATATTAAGAG	GTGCTCTGAG	ATGATGCTTG	ACACTTTTC	ATTTAGGATC	ACATCTACAT	TCAATGCTAC	ATACGTGACA
6110	6120	6130	6140	6150	6160	6170	6180	6190	6200
GACTTCTCAA	TGATTAATGC	AAATATTGTA	CATCTAACGTC	CTCTAGACTT	GTCAAATCAA	ATCAATTCAA	AAAACAAATC	TCTTAAAAGT	GCTGAGGATT
6210	6220	6230	6240	6250	6260	6270	6280	6290	6300
GGATTGCAGA	TAGCAACTTC	TTCGCTAATC	AAGCCAGAAC	AGCCAAGACA	CTTTATTCA	TAAGTGCAT	CGCATTAATA	CTATCAGTGA	TTACTTTGGT
6310	6320	6330	6340	6350	6360	6370	6380	6390	6400
TGTTGTGGGA	TTGCTGATTG	CCTACATCAT	CAAGCTGGT	TCTCAAATCC	ATCAATTCA	AGCAGTAGCT	GCTACAACAA	TGTTCCACAG	GGAGAATCCT
6410	6420	6430	6440	6450	6460	6470	6480	6490	6500
GCCGTCTTT	CCAAGAACAA	TCATGGAAC	ATATATGGGA	TATCTTAAAG	ATTCTATCAT	AAGTCCATAT	ATGTCCATGA	TTGACCTTTA	AGAGCCAAC
6510	6520	6530	6540	6550	6560	6570	6580	6590	6600
TCCAATGATT	ATCCGTTAAA	TTCAGATATA	ACAATTCAA	AATCAATT	AAGCCTCCAG	ATACCAATGA	ATATGAATAT	ATCTCTTAGA	AAACTTGATT
6610	6620	6630	6640	6650	6660	6670	6680	6690	6700
ATTATGTGAT	AACATAGTAC	AATTTAAGAA	AAAACCTAA	ATAAGCACGA	ACCCCTAAGG	TGTCGTAAAG	TCTCGTGACG	CCGGGTTCA	TTCAAAACATC
6710	6720	6730	6740	6750	6760	6770	6780	6790	6800
GACCCCTGAC	CCAATTCAAT	ACCCATTTC	ATAAGGAAC	ACAGTATAAT	TTAACATCAA	AAGACCTCAA	AATCTGATAC	AGCTTAATCC	ACTCAACATA
6810	6820	6830	6840	6850	6860	6870	6880	6890	6900
TAATTATAAG	ACTAATAATA	ATGGAAGATT	ACAGCAATCT	ATCTCTTAA	TCATTCTCA	AAAGGACATG	TAGAACATT	TTCCGAAC	CCACAATTCT
6910	6920	6930	6940	6950	6960	6970	6980	6990	7000
TGGCATATGC	ACATTAATTG	TGCTATGTC	AAGTATTCTT	CATGAGATA	TTCATCTTGA	TGTTCTCT	GGTCTTATGA	ATTCTGATGA	GTCACAGCAA
7010	7020	7030	7040	7050	7060	7070	7080	7090	7100
GGCATTATTTC	AGCCTATCAT	AGAATCAITTA	AAATCATTGA	TTGCTTTGGC	CAACAGATT	CTATATAATG	TTGCAATAGT	AATTCTCTT	AAATTGACA
7110	7120	7130	7140	7150	7160	7170	7180	7190	7200
GTATCGAAAC	TGTAATACTC	TCTGCTTAA	AAGATATGCA	CACCGGGAGT	ATGTCCAATG	CCAACTGCAC	GCCAGGAAAT	CTGCTTCTGC	ATGATGCAGC
7210	7220	7230	7240	7250	7260	7270	7280	7290	7300
ATACATCAAT	GGAATAAAACAA	AATTCTCTGT	ACTTGAATCA	TACAATGGGA	CGCCTAAATA	TGGACCTCTC	CTAAATATAC	CCAGCTTTAT	CCCCTCAGCA
7310	7320	7330	7340	7350	7360	7370	7380	7390	7400
ACATCTCCC	ATGGGTGTAC	TAGAATACCA	TCATTTTCAC	TCATCAAGAC	CCATTGGTGT	TACACTCACA	ATGTAATGCT	TGGAGATTGT	CTTGATTTCA
7410	7420	7430	7440	7450	7460	7470	7480	7490	7500
CGGCATCTAA	CCAGTATTAA	TCATGGGGA	TAATACAAACAA	ATCTCTGCA	GGGTTTCCAA	TTTCAGGAC	TATGAAAACC	ATTTACCTAA	GTGATGGAAT
7510	7520	7530	7540	7550	7560	7570	7580	7590	7600
CAATCGAAAC	AGCTGTTCA	TCACTGCTAT	ACCAAGGAGT	TGTGTCTGT	ATTGCTATGT	AGCTACAAGG	TCTGAAAAAG	AAGATTATGC	CACGACTGAT
7610	7620	7630	7640	7650	7660	7670	7680	7690	7700
CTAGCTGAAC	TGAGACTTGC	TTTCTATTAT	TATAATGATA	CCCTTATTGA	AAGAGTCATA	TCTCTTCCAA	ATACAAACAGG	GCAGTGGGCC	ACAATCAACC
7710	7720	7730	7740	7750	7760	7770	7780	7790	7800
CTGCAGTCGG	AAGCGGGATC	TATCATCTAG	GCTTTATCTT	ATTCCCTGTA	TATGGTGGTC	TCATAAAATGG	GACTACTCT	TACAATGAGC	AGTCCTCACG
7810	7820	7830	7840	7850	7860	7870	7880	7890	7900
CTATTCTTATC	CCAAAACATC	CCAACATAAC	TTGTCGGGT	AACTCCAGCA	AACAGGCTGC	AATAGCACGG	AGTTCCCTATG	TCATCCGTTA	TCACTCAAAC
7910	7920	7930	7940	7950	7960	7970	7980	7990	8000
AGGTAAATTG	AGAGTGTG	TCTTATTGTTG	CCATTGTC	ACATGCATAC	AGAAGAGTGT	AATCTAGTTA	TGTTAAACAA	TTCCCAAGTC	ATGATGGGTG
8010	8020	8030	8040	8050	8060	8070	8080	8090	8100
CAGAAGGTAG	GCTCTATGTT	ATTGTTAATA	ATTGTTAATA	TTATCAACGC	AGTTCCCTTT	GGTGGTCTGC	ATCGCTCTTT	TACAGGATCA	ATACAGATT
8110	8120	8130	8140	8150	8160	8170	8180	8190	8200
TTCTAAAGGA	ATTCCTCCGA	TCATTGAGGC	TCAATGGGT	CCGCTCTATC	AAGTTCCCTCG	TCCTGGAGTC	ATGCCATGCA	ATGCAACAAAG	TTTTGCGCT
8210	8220	8230	8240	8250	8260	8270	8280	8290	8300
GCTTAATTGCA	TCACAGGGGT	GTACCGCAGAT	GTGTGGGCC	TTAATGATCC	AGAACTCATG	TCACGTAATG	CTCTGAACCC	CAACTATCGA	TTTGTGGAG
8310	8320	8330	8340	8350	8360	8370	8380	8390	8400
CCTTTCTCAA	AAATGAGTCC	AACCGAACTA	ATCCCACATT	CTACACTGCA	TCGGCTAACT	CCCTCTTAA	TAACCTGGGA	TTCACAAACAA	CCAATCACAA
8410	8420	8430	8440	8450	8460	8470	8480	8490	8500
AGCAGCCATAT	ACATCTCAA	CCTGTTAA	AAACACTGGA	ACCCAAAAAA	TTTATTGTTT	AATAATAATT	GAAATGGGCT	CATCTCTTT	AGGGGAGTTC
8510	8520	8530	8540	8550	8560	8570	8580	8590	8600
CAAATAATAC	CATTTTAAG	GGAACAAATG	CTTAAATCCT	ATTGAATGAA	GACTCCAGAT	TCAAGAAATAA	TTGGAAGGCT	CTTTATTTTA	TGCGATAGTT
8610	8620	8630	8640	8650	8660	8670	8680	8690	8700
ATACGTTTTG	GCTGTATTAG	AATGCTATAG	CATTCTGCTG	TTTTCCCAT	ATGGAAAAAT	CCTTCAACAC	CAACTTAGGT	TCAATTCT	CATCATTTAC

FIGURE 9C

8710	8720	8730	8740	8750	8760	8770	8780	8790	8800
TGTTGTAATT	CAATCTTACT	AAAGTTATTTC	TGATATTAA	GAAAAAATAA	TCTTTATATA	ATGTAACAAT	ACTACTAAGA	TTATAATATA	GGCCAGAATG
8810	8820	8830	8840	8850	8860	8870	8880	8890	8900
GCAGGCCTCTT	CTGAGATACT	CCTTCCTGAA	GTCCATTGAA	ACTCACCAAT	AGTCACAC	AAACTCATAT	ACTACTATAT	ACTAGGGCAC	TTCCCGCATG
8910	8920	8930	8940	8950	8960	8970	8980	8990	9000
ATCTTGACAT	TTCTGAAATA	AGCCCCCTTC	ACAATAATGA	TTGGGATCAG	ATTGCCAGAG	AAGAATCCAA	TCTTGCTGAA	CGACTCGGAG	TAGCTAAATC
9010	9020	9030	9040	9050	9060	9070	9080	9090	9100
TGAATTAATT	AAACGTGTGC	CCGCATTAG	AGCAACCAGA	TGGCGTAGTC	ATGCAGCCGT	CCTTATATGG	CCTTCTTGAA	TACCATTCCT	TGTTAAATTC
9110	9120	9130	9140	9150	9160	9170	9180	9190	9200
CTACCCCATT	CTAACGCTCA	ACCAATGAA	CAATGGTACA	AGTTGATCAA	TGTTCATGC	AATACTATAT	CTGACTCAAT	TGATAGATGT	ATGGAGAATA
9210	9220	9230	9240	9250	9260	9270	9280	9290	9300
TTTCTATTAA	GCTTACTGGG	AAAACAATC	TATTCTCTCG	ATCCAGAGGA	ACTGCAGGCG	CAGTAAAAAA	CAGTAAATC	ACCCCTCAATG	ATATCCAATC
9310	9320	9330	9340	9350	9360	9370	9380	9390	9400
TATTTGGAA	TCAAACAAAT	GGCAGCCTAA	TGTATCTTA	TGGCTTACAA	TTAAATACCA	AATGCGACAA	CTTATAATGC	ATCAAAGTTC	TCGTCAGCCA
9410	9420	9430	9440	9450	9460	9470	9480	9490	9500
ACTGATTTAG	TTCACATTGT	TGACACACGA	TCTGGTCTAA	TAGTTATCAC	CCCTGAACCT	GTTATTGCT	TTGATCGGTT	GAATAATGTT	TTAATGTATT
9510	9520	9530	9540	9550	9560	9570	9580	9590	9600
TTACATTGAA	GATGACTTTA	ATGGTAAGTG	ACATGTTGA	GGGACGGATG	AATGTTGCCG	CGCTCTGCAC	TATTAGTCAT	TACTTATCAC	CACTAGGGCC
9610	9620	9630	9640	9650	9660	9670	9680	9690	9700
AAGGATAGAT	AGATTGTTTT	CTATTGAGA	TGAATTAGCA	CAACTATTGG	GTGACACTGT	ATATAAAATT	ATTGCACTTC	TTGAATCTTT	AGTATATGGG
9710	9720	9730	9740	9750	9760	9770	9780	9790	9800
TGCTCTAACAC	TTAAAGATCC	AGTGGTTGAA	TTAACAGGAT	CATTTCATTC	CTTTATTAGC	CAAGAGATTA	TAGATATCCT	AATTGGTCA	AAAGCCCTTG
9810	9820	9830	9840	9850	9860	9870	9880	9890	9900
ATAAGGATGA	ATCAATAACT	GTCACTACAC	AATTGCTAGA	TATATTTTC	AACTTTTCTC	CAGATTTAAT	CGCTGAGATG	TTGTGCTCA	TGAGACTTTG
9910	9920	9930	9940	9950	9960	9970	9980	9990	10000
GGGTCACTCCC	ACTCTTACTG	CTGCGCAAGC	TGCAGGTAAA	GTGAGAGAA	CTATGTTGTC	AGGTAAGTTA	CTTGATTTCC	CTACAATAAT	GAAAACCTTT
10010	10020	10030	10040	10050	10060	10070	10080	10090	10100
GCTTTTTTCC	ACACAATTTT	AATCAATGGT	TATCGTAGAA	AGAAGAAATGG	AATGTTGCC	CCACTTATAC	TTCCCTAAAAA	TGCACTAAAAA	ACCTTAATAG
10110	10120	10130	10140	10150	10160	10170	10180	10190	10200
AGTTTCAACA	TGATAATGCT	GAATATCTT	ATGAGTATAC	ACTCAAGCAT	TGGAAAGAAA	TCTCTCTCAT	AGAATTAGA	AAGTGCTTTG	ACTTTGATCC
10210	10220	10230	10240	10250	10260	10270	10280	10290	10300
TGGTGAGGAG	CTAACGATT	TTATGAAAGA	CAAGGCAATA	AGTGTCCAA	AAAGTGTATTG	GATGAGTGTAA	TTCCGTAGAA	GTCTAATAAA	ACAAAGCACAT
10310	10320	10330	10340	10350	10360	10370	10380	10390	10400
CAGAGACATC	ATATTCCAT	GCCCAATCCA	TTAACAGAC	GTCTATTACT	CAATTCTTA	GAAGATGACA	GTTTGATCC	AGTTGCTGAG	CTTCAATATG
10410	10420	10430	10440	10450	10460	10470	10480	10490	10500
TTACCCAGTGG	TGAATATCTC	CGAGATGACA	CATTTGTGC	ATCTTACTCA	TTAAAGAGA	AAGAAATAAA	ACCAAGATGGA	AGGATATTG	CTAACGTTAC
10510	10520	10530	10540	10550	10560	10570	10580	10590	10600
TAATAGAATG	CGGTCTTGTC	AAGTAATTG	GGAAGCAATT	CTTGCAAATC	ACGCAGGTAC	TCTAATGAAG	GAAAACGGAG	TTGTCTTGAA	TCAATTATCT
10610	10620	10630	10640	10650	10660	10670	10680	10690	10700
CTGACTAAAT	CATTGCTTAC	TATGAGTCAA	ATTGGCATAA	TATCAGAAAAA	AGCAAAGAGA	TATACCCGAG	ATAACATCTC	ATCTCAAGGT	TTCCATACAA
10710	10720	10730	10740	10750	10760	10770	10780	10790	10800
TCAAGACTGA	CTCAAAAAAT	AAGAAGAAA	GCAAAATTG	ATCATCATAC	CTCACAGATC	CTGATGATAC	ATTGAACTT	AGTGCATGTT	TTATAACTAC
10810	10820	10830	10840	10850	10860	10870	10880	10890	10900
TGACTCTGCT	AAATACTGTC	TTCAATGGG	ATACAGAC	ATAATCCATT	TTGCTCGAAC	ATTAACAGAG	ATGTATGGAG	TTCCACATTT	ATTGAATGG
10910	10920	10930	10940	10950	10960	10970	10980	10990	11000
ATTCAATCTTC	GTTTGATTAG	ATCTACATTA	TATGTTGGT	ATCCATTCAA	TCCTCTTGCC	ACAACTGATG	CCTTCGATCT	AGATAAAGTA	TTAAATGGT
11010	11020	11030	11040	11050	11060	11070	11080	11090	11100
ATATCTTAT	AGTCCTCTCC	AGGGAGGTA	TTGAAGGCCT	ATGTCAGAAA	ATGTGGACAA	TGATCTCTAT	TTCTGTGATC	ATCCTTTCTT	CAGCCGAATC
11110	11120	11130	11140	11150	11160	11170	11180	11190	11200
CAAAACAAGA	GTAATGAGCA	TGGTCAAGG	AGATAATCAG	GCGATTGCG	TTACAACAAAG	AGTTCCTAGA	TCATTGCCAA	GTGTTCAAGAA	AAAGGAGTTA
11210	11220	11230	11240	11250	11260	11270	11280	11290	11300
GCCTACGAG	CAAGCAAGTT	ATTCTTGGAA	AGACTTAGGG	CAAATAATTG	TGGTTGGGT	CATCAACTAA	AGGCTCAAGA	GACTATAATA	AGTTCCACGT
11310	11320	11330	11340	11350	11360	11370	11380	11390	11400
TCTTCATATA	TAGTAAACGG	GTATTCTATC	AAGGACGTAT	ACTAACACAG	GCACCTAAAAA	ATGCTAGCAA	GTATGTCCTT	ACTGCAGATG	TATTAGGTGA
11410	11420	11430	11440	11450	11460	11470	11480	11490	11500
ATGTACTCAG	GCTTCCTGCT	CAAATTCTGC	TACTACAATC	ATGAGATTAA	CAGAAAATGG	GGTTGAGAAA	GATACATGTT	ATAAGCTTAA	TATTATCACAA
11510	11520	11530	11540	11550	11560	11570	11580	11590	11600
TCTATTGCTC	AACTCACATA	TGATCTAATA	TTTCCCAAT	ACTCCATACC	AGGTGAAACA	ATAAGTGA	TTTCTTACAA	GCATCCAAGA	TTAATCTCAC

FIGURE 9D

11610	11620	11630	11640	11650	11660	11670	11680	11690	11700
GTATTGTTCT	GCTCCCTTCA	CAGCTAGGTG	GTCTTAATTA	CCTCGCATGT	AGCAGATTAT	TTAACCGCAA	TATCGGAGAT	CCCCCTGGTA	CAGCCGTGGC
11710	11720	11730	11740	11750	11760	11770	11780	11790	11800
AGACCTCAAG	AGGTTAATTA	AATGTGGTGC	TCTTGAATCA	TGGATACTGT	ACAATTACT	GGCAAGAAA	CCAGGGAAAG	GTTCATGGGC	CACTTTAGCA
11810	11820	11830	11840	11850	11860	11870	11880	11890	11900
GCCGATCCAT	ACTCATGAA	TCAAGAATAT	CTTTATCCTC	CTACTACTAT	ACTTAAAAGA	CATACTCAA	ATACTTTAA	GGAGATATGT	CGGAATCCTA
11910	11920	11930	11940	11950	11960	11970	11980	11990	12000
TGTTAAAGGG	AGTTTTACA	GATAATGCAA	AAGAGGAGGA	AAATCTCCTT	GCAAAATTTC	TTCTTGATCG	TGATATAGTA	TTGCCAAGAG	TCGCACACAT
12010	12020	12030	12040	12050	12060	12070	12080	12090	12100
TATAATAGT	CAATCCAGCA	TTGGAAGGAA	GAAACAGATA	CAAGGGTTT	TTGACACCAC	AAGGACCATA	ATGAGACGAT	CATTTGAGAT	CAAACCACTC
12110	12120	12130	12140	12150	12160	12170	12180	12190	12200
TCAACTAAGA	AGACACTTTC	AGTCATAGAA	TATAAATACTA	ATTATTTATC	TTATAACTAC	CCTGTCATAC	TTAACCTTT	ACCTATTCC	GGATATTTAA
12210	12220	12230	12240	12250	12260	12270	12280	12290	12300
ATTATATTAC	TGACCAAACT	TGCGATTTG	ATATATCTAG	AAGTTAAAGA	AAATTATCAT	GGTCTTCTTT	ATTGAATGGA	AGAACTTTAG	AAGGATTAGA
12310	12320	12330	12340	12350	12360	12370	12380	12390	12400
AACTCCAGAT	CCAATTGAA	TTGTCATGG	TTCTTGTATT	GTAGGTACAG	GAGATTGTGA	CTTTTGTATG	CAGGGTGACG	ATAAATTCA	TTGGTTCTTT
12410	12420	12430	12440	12450	12460	12470	12480	12490	12500
TTACCTATGG	GGATAATTAT	TGATGAAAT	CCTGAAACTA	ATCCACCCAT	CAGAGTTCCA	TACATTGGGT	CTAGAACAGA	GGAAAGAAGA	GTTGCATCAA
12510	12520	12530	12540	12550	12560	12570	12580	12590	12600
TGGCATATAT	TAAGGGTGC	ACACACAGTT	TGAAGGGTGC	TCTTAGAGGC	CGAGGGTAT	ACATTTGGGC	ATTCGGAGAT	ACAGTAGTGA	ACTGGAAATGA
12610	12620	12630	12640	12650	12660	12670	12680	12690	12700
TGCACTTGAT	ATCGAAATA	CTAGGGTTAA	GATATCCCTA	GAGCAACTTC	AGACTCTTAC	ACCTCTTCC	ACATCTGAA	ACATTACACA	TCGTTTAGAT
12710	12720	12730	12740	12750	12760	12770	12780	12790	12800
GATGGAGCCA	CAACACTTAA	ATTCACCTCA	GCTAGTTCT	ATGCATTTTC	TAGTTTACT	CATATATCAA	ATGATCAACA	ATATTTAGAA	ATAGATCAGA
12810	12820	12830	12840	12850	12860	12870	12880	12890	12900
GAGTAGTCGA	TTCCAATATT	ATTATCAAC	AATTAATGAT	AACAGGGCTT	GGGATCATTG	AGACCTACCA	TAACCCACT	ATCAGGACCT	CTACACAGGA
12910	12920	12930	12940	12950	12960	12970	12980	12990	13000
AATCACCCCTC	CATTGCAACA	CTAGCTCATC	TTGTTGTGTT	AGAAGGTGAG	ATGGTTGCCT	TATATGTGAG	AGCAATGGAG	AGGTTCCCTCA	GATCACTGTT
13010	13020	13030	13040	13050	13060	13070	13080	13090	13100
CCCTACACTA	ATTCATTTGT	ATATGATCCT	GATCCACTAG	CAGATTATGA	GATTGCACAT	CTAGATTATC	TCTCCTACCA	AGCTAAAATT	GGAAGTACAG
13110	13120	13130	13140	13150	13160	13170	13180	13190	13200
ATTACTACTC	ACTTACTGTAT	AAAATTGATC	TATTGGCACA	TTTAACTGCA	AAACAAATGA	TAAACTCAAT	AATTGGGTTA	GATGAAACAG	TATCAATTGT
13210	13220	13230	13240	13250	13260	13270	13280	13290	13300
CAATGATGG	GTTTATCTAT	CTGATTATAC	TAATAACTGG	ATTAGTGAAT	GTTCTTATAC	TAAGATAGAT	TTAGTTTTA	AATTAATGGC	ATGGAATTTC
13310	13320	13330	13340	13350	13360	13370	13380	13390	13400
CTTCTTGAGC	TTGCATTCCA	GATGTAATAC	CTAAGAAATAT	CATCTGGAC	AAATATATT	GACTATACTT	ACATGACTT	ACGCAGGATA	CCCGGAACGT
13410	13420	13430	13440	13450	13460	13470	13480	13490	13500
CTCTAACATAA	TATTGAGGCC	ACCCAAATT	ATTAAGACGT	GCAATGAATC	TTGATATTAT	CACTCCCTATA	CATGCACCGT	ATTTGGCTTC	
13510	13520	13530	13540	13550	13560	13570	13580	13590	13600
ATTAGATTAT	GTCAAATTAA	GTATTGATGC	AATTCACTGG	GGGGTTAAAC	AAGTTCTTGC	TGATTTATCA	AATGGAATTG	ATCTTGAAT	CTTGATTCCT
13610	13620	13630	13640	13650	13660	13670	13680	13690	13700
TCAGAGGATT	CAATGGAAAT	TAGTGAATGG	GCAATGAATC	TCATTGCTAG	AAAACTAATC	CTCCTTGAC	TTGTTAAAGG	TGAGAACTAT	ACATTTCCAA
13710	13720	13730	13740	13750	13760	13770	13780	13790	13800
AAATTAAAGG	GATGCCACCA	GAGGAAAGT	GTTCAGTCTT	AACTGAATAT	CTAGCAATGT	GTTATCAGAA	TACTCACCAC	TTAGATCCAG	ATCTTCAAA
13810	13820	13830	13840	13850	13860	13870	13880	13890	13900
GTATTATAT	AATCTAACTA	ATCCAAATT	GACTGCATTT	CCCAGTAACA	ACTCTACTT	AACAAAGAAA	ATCCTTAATC	AAATTAGAGA	ATCAGACGAA
13910	13920	13930	13940	13950	13960	13970	13980	13990	14000
GGACAAATATA	TTATCACCTC	ATATTATGAA	TCCTTCGAAC	AATTAGAAAC	AGATATAATT	CTTCACCTCA	CTTTAACATGC	TCCTTATGAT	AATTCAGAAA
14010	14020	14030	14040	14050	14060	14070	14080	14090	14100
CTCTAACAAA	GTTTGTATTA	TCCCTTGAC	TCTTCCACA	TCCAGAAATCT	CTCGAGAAAT	ATCCTCTTCC	AGTTGATCAT	GACTCTCAAT	CTGCAATTTC
14110	14120	14130	14140	14150	14160	14170	14180	14190	14200
AACACTAATT	CCAGGCCCTC	CCTCTCATCA	TGTATTACGA	CCACTAGGAG	TGTCATCTAC	AGCTTGGAT	AAAGGGATAA	GTTATTGCG	ATACCTGGAA
14210	14220	14230	14240	14250	14260	14270	14280	14290	14300
ACGCAAAAGA	TACAGACTGG	TGATCATCTT	TATTAGCTG	AAGGAAGCGG	TGCTTCAATG	TCACTCTTAG	AACTCCTATT	TCCAGGAGAT	ACTGTCATT
14310	14320	14330	14340	14350	14360	14370	14380	14390	14400
ATAATAGTCT	TTTTAGTAGT	GGAGAGAAATC	CTCCACAGAG	AAATTATGCT	CCTCTTCCAA	CTCAATTGTT	ACAGAGTGT	CCATATAAAT	TGTGGCAAGC
14410	14420	14430	14440	14450	14460	14470	14480	14490	14500
TGATCTTGCT	GATGATAGTA	ACTTAATAAA	AGATTTGTC	CCATTATGGA	ATGGAACCGG	AGCAGTTACA	GACTTATCGA	CAAAGGATGC	AGTTGCAATT

14510	14520	14530	14540	14550	14560	14570	14580	14590	14600
ATAATACATA	AAGTAGGAGC	GGAGAAAAGCA	TCCCCTTGTTC	ATATAGATCT	CGAACGACT	GCTAAATATAA	ATCAGCAAAC	TCTGTCCAGA	TCCCAGATT
14610	14620	14630	14640	14650	14660	14670	14680	14690	14700
ATTCGTTAAT	TATAGCAAATC	ACTGTTCTTA	AGAGGGGTGG	GATATTAGTT	TACAAAACAT	CATGGCTTCC	GTTCCTAGG	TTTAGTCAC	TAGCAAGCCT
14710	14720	14730	14740	14750	14760	14770	14780	14790	14800
ACTTTGGTGC	TTTTTGACC	GGATCCATCT	AATACGTA	AGTTATTCTG	ATCCTCACAG	TCATGAGGTT	TATCTGTAT	GTAGACTTGC	TGCGGATTT
14810	14820	14830	14840	14850	14860	14870	14880	14890	14900
AGAACTATCG	GTTTCAGTGC	AGCTCTAGTA	ACTGCTACTA	CTCTTCACAA	TGACGGATT	ACAACAATAC	ATCCTGATGT	TGTTTGAGT	TATTGGCAAC
14910	14920	14930	14940	14950	14960	14970	14980	14990	15000
ACCATCTTGA	GAATGTTGGG	AGAGTCGAAA	AAGTAATTGA	TGAGATACTT	GATGGTTAG	CCACCAACTT	CTTCGCAGGA	GATAATGGGC	TTATTCTAAG
15010	15020	15030	15040	15050	15060	15070	15080	15090	15100
ATGTGGAGGA	ACTCCCAGCT	CTAGAAAATG	GTTAGAGATT	GATCAGTTAG	CATCATTTGA	TTCAGTTCAA	GATGCTCTAG	TGACACTTAT	CACCATAAC
15110	15120	15130	15140	15150	15160	15170	15180	15190	15200
CTAAAGGAAA	TTATAGAAAGT	GCAGTCATCA	CATACAGAGG	ATTATACATC	TCTCCTTTTC	ACACCTTATA	ATATTGGTGC	AGCAGGGAAA	GTAAGAACTA
15210	15220	15230	15240	15250	15260	15270	15280	15290	15300
TCATCAAATT	AATTCTAGAA	CGATCTTAA	TGTATACAGT	CCGAAATTGG	TTAGTTTTAC	CCAGTTCCAT	CCGGGATTCC	GTACGACAAG	ATCTAGAGTT
15310	15320	15330	15340	15350	15360	15370	15380	15390	15400
AGGGTCATTT	AGATTAATGT	CTATTTAAG	TGAACAGACA	TTCTTAAAAA	AGACACCCAC	CAAAAAATAC	TTACTTGATC	AGCTTACAAG	GACATATATA
15410	15420	15430	15440	15450	15460	15470	15480	15490	15500
TCAACCTTCT	TTAATTCTCA	CTCAGTCCTC	CCCCCTCCACC	GTCCCATATCA	AAAACAAATA	TGGAAAGCCT	TAGGTAGTGT	AATATATTGT	TCGGAGACGG
15510	15520	15530	15540	15550	15560	15570	15580	15590	15600
TTGATATACC	TCTAATTAGA	GACATTCAGA	TAGAAGATAT	TAATGATTT	GAAGATATCG	AGAGGGTAT	CGATGGCGAA	GAATTATGAC	AACAGTGATT
15610	15620	15630	15640	15650					
ATAAGAAACTC	ATGATAGTT	TATTTAAGAA	AAACATATTG	ATTTTCCCT	TGGT				

Human Parainfluenza Virus Type 2 Strain V98 Antigenomic sense cDNA Sequence Range: 1 to 15654

10	20	30	40	50	60	70	80	90	100
ACCAAGGGGA	GAATTAGATG	GCATCGTTAT	ATGACGAATT	GCAAAAGAT	TACGTAGGTC	CGGAACCACT	AGATTCCGGT	GCCGTTAACG	ATTCCATTTC
110	120	130	140	150	160	170	180	190	200
TATACTATCT	GATCATTCTC	TATCTCTACT	AAGGATATT	CTAGTCTAAA	GTTCAAATG	TCAAGTGTCT	TAAAGACATT	TGAAAGGTTT	ACTATACAAC
210	220	230	240	250	260	270	280	290	300
AAGAGCTTCA	GGAGCAATCT	GATGACACTC	CAGTACCTCT	TGAGACAATC	AAACCTACAA	TAAGGGTATT	TGTCAATCAAT	AATAATGATC	CTGCCATAAG
310	320	330	340	350	360	370	380	390	400
GCTTAGACTT	TTATTCTTTA	ATCTACGAAT	TATTATGAGT	AACACCGCAA	GAGAGGGACA	TAGAGCTGTT	GCTCTCTCA	GTCTCTTATC	ACTACCTCT
410	420	430	440	450	460	470	480	490	500
GCAGCTATGA	GTAATCACAT	CAAACATAGCC	ATGCATTTCAC	CAGAAGCCAG	CATAGATAGA	GTAGAGATAA	CAGGGTTGAA	GAATAATTCA	TTCCGAGTTA
510	520	530	540	550	560	570	580	590	600
TTCCAGATGC	TCGATCAACT	ATGTCAGAG	GAGAGGTGCT	GGCCTTTGAA	GCATTAGCTG	AAGACATTCC	TGATACCCTT	AATCACCAAA	CTCCATTGTT
610	620	630	640	650	660	670	680	690	700
AAATAATGAT	GTAGAAAGATG	ACATGTTGAA	TGAAACAGAG	AAATTCTTAG	ATGTTTGCTA	CAGTGTACTT	ATGCAGGCAT	GGATAGTAAC	ATGCAAGTGT
710	720	730	740	750	760	770	780	790	800
ATGACTGCTC	CTGATCAGCC	GCCAGTATCA	GTAGCAAAAGC	GGATGGCTAA	ATATCAACAA	CAAGGGAGAA	TCAATGCTAG	GTATGTACTA	CAGCCTGAAG
810	820	830	840	850	860	870	880	890	900
CACAAAGACT	AATTCAAGAT	GCCATCCGCA	AGTCATGGT	AGTGAGGCAT	TTCATGACTT	ATGAGCTTCA	ACTTCACAA	TCAAGATCTT	TGCTAGCAA
910	920	930	940	950	960	970	980	990	1000
CCGCTACTAT	GCTATGGTGG	GAGACATTG	CAAGTACATT	GAACACAGCG	GAATGGGAGG	TTTTTCTTA	ACACTTAAAT	ATGGACTTGG	AACAAGATGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
CCTACATTGG	CTCTTGCGAC	ATTCTCTGG	GAACCTCAGA	AATTAAAAGC	TCTCATGCTA	CATTATCAGA	GCCTAGGACC	CATGGCCAAG	TACATGGCTC
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TATTAGAATC	ACCAAAGCTG	ATGGATTTTG	TCCCACATG	ATATCAATT	GTTTATAGTT	ATGCAATGGG	TATTGGAACT	GTCTTGATA	CAAATATGAG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AAACTATGCA	TATGGTAGAT	CATATTTAA	TCCGCAATAT	TTTCAGCTAG	GAGTAGAAAC	AGCAAGGAAA	CAGCAGGGAG	CTGTTGACAA	CAGGACAGCA
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
GAGGACCTCG	GCATGACTGC	TGCAAGACAA	GCAGACCTCA	CTGCAACCAT	ATCAAAGCTA	TCTTTGTC	AATTACCTAG	GGGTAGACAA	CCAATATCTG
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ACCCATTGTC	TGGAGCAAAT	GACAGAGAAA	TAGGAGGCCA	AGCAAATGAT	ACACCTGTAT	ACAACTTCAA	TCCAATCAAT	ACTCGGAGGT	ATGACAACTA
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
TGACAGTGT	GGTGAGGACA	GAATTGACAA	CGATCAAGAT	CAAGCTATCA	GAGAGAACAG	AGGAGAGCCT	GGACAACATAA	ACAACCAGAC	AAVTGACAAC
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
CAGCAGAGAC	TCAATCTCTC	CATACCGCAA	AGAACATCG	GTATGAGCAG	TGAAGAGTTC	CAACATTCAA	TGAATCAGTA	CATCCGTGCC	ATGCATGAGC
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
AATACAGAGG	ACCCCAGGAT	GATGATACCA	ATGATGCCG	AGATGGGAAT	GACATTCTC	TTGAGCTAGT	TGGGATTTT	GATTCTTAAT	TCTCAATGTC
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
ATACAACCAG	ATATACACAT	CCACATCACT	TAAGATACA	GCTGCCACCC	ACACACTCAT	CCAGACAAAT	CAAACCCAGAC	TCACATCATT	CAGAAACAAAT
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
TCTCTCATAA	TTAAAGAAAA	AAACATAGGC	CCGGACGGGT	TTAAAATCTG	GTGCTCGTTC	GTGGCTGAC	AACCTCCAAA	CCAGAACATC	ACAATTATGG
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
CCGAGGAACC	AACATACACC	ACTGAGCAAG	TTGATGA	ATCCATGCT	GGACTGGAA	CAGTAGATT	CTTCCTATCT	AGACCCATAG	ATGCTCAATC
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TTCCCTAGGC	AAGGGCAGCA	TCCCCACAGG	TGTCACAGCT	GTTCTAACTA	GTGCAGCAGA	GGCAAATCTC	AAACCACTG	CCGCTGGTCC	AGTGAACACC
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
AGGGCGGAAAGA	AAGTGTACAG	CAATGCTACC	CCATACACTG	TTGCAGACAA	TACTCCACCT	GAGAAGCTAC	CAATCAACAC	CCCAATACCC	AATCCATTAC
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
TTCCACTGGC	ACGGCCCCAA	GGAAAGATGA	CAGACATTGA	CATTGTCACT	GGGACCATTA	CAGAAGGATC	GTACAAAGGT	GTGGAGCTTG	CTAAATTAGG
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
GAAGCAAAAC	CTACTCACAA	GGTTCACCTC	GAACGAGCCA	GTCTCCTCG	CTGGATCCGC	CCAAGACCCC	AACTTTAAAGA	GGGGGGGAGC	TAATAGAGAA
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
AGAGCAAGAG	GCAACCATAG	GAGAGAATGG	AGTATTCAT	GGGTCGGAGA	TCAGGTCAA	GTCTTCGAGT	GGTGTAAATCC	CAGGTGTGCC	CCAGTCACGG
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
CCTCAGCTCG	CAAGTTCAACC	TGCACATGCG	GATCCCTGCC	CAGCATCTGC	GGAGAATGTC	AAGGAGATCA	TTGAGCTCTT	AAAGGGGCTT	GATCTTCGCC
2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
TTCAGACTGT	AGAAGGGAAAG	GTAGATAAAA	TTCTTGCAAC	TTCCGCAACT	ATAATCAATC	TTAAAAATGA	AATGACTAGT	CTCAAGGGCA	GCGTTGCAAC
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
TGTGGAAGGT	ATGATAACAA	CAATTAAAAT	CATGGATCCC	AGCACACCAA	CCAATGTCCC	TGTAGAGGAG	ATCAGAAAGA	GCTTACACAA	TGCTCCAGTA

FIGURE 10A

2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
GTAATTGCCG	GTCCAACTAG	TGGAGGCTTC	ACAGCCGAAG	GCAGTGATAT	GATTTCAATG	GATGAACCTAG	CTAGACCTAC	ACTCTCATCA	ACAAAAAAGA
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
TCACACGAAA	GCCTGAATCC	AAGAAAGACT	TAACAGGCAC	AAAACAAACC	TTGATGCAGC	TTGCAAATGA	CTGCATCTCG	CGTCCAGATA	CCAAGACTGA
3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
GTCGTGACT	AAGATTCAAG	CAGCAACCAC	AGAACATCACAG	CTTAATGAAA	TCAAGCGGTC	AATAATACGC	TCTGCAATAT	AAAATGAGGT	GCAATCACAC
3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
AAGAGACACT	AAACATGCAT	CCAATCAAGA	TCCAAATTCT	GTCCATCCGA	AAACACACCC	ACAATTGTTA	ACACCAAGAA	ACAACCACAG	CCGAACCATG
3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
CTTAATCAAA	AGATCCAAAC	AAACATCTCAC	ATCGACAGAA	GGCTGGACAT	GATAAATTAA	ATAAAAAAAGA	AAAAAAAGTC	AAGTAAAATT	TAAAGGACAC
3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
AATAGAGAAA	ATCTAGGTCC	GAAAGCTTGC	TTCCCGGACA	GATCTCAAAA	TCATAGTCTA	AACCTCAAC	ACAGCAGCAC	ACATGCCAT	AATATCATTA
3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
CCAGCAGATC	CAACTTCACC	CAGTCATACC	CTTACTCCGT	TTCCAATACA	ACTTGACACC	AAAGATGGCA	AGGCAGGGAA	ACTCCTTAAA	CAGATTGCAA
3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
TTAGGTATCT	AAATGAGCCT	ATTCTCGCC	ATACACCAAT	AACTTCATC	AATACGTATG	GATTGTTTA	TGCTCGAGAC	ACTTCAGGGG	GCATTACACAG
3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
TGAGCTTAGT	AGTGACCTAG	CTGCAGGGTC	TATAACAGCA	TGCATGATGA	CGCTAGGCC	TGGTCCAAAT	ATTCTAGATG	CAAATCTAGT	GCTAAGATCT
3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
CTGAATGAAT	TCTACGTGAA	AGTCAAGAAAG	ACATCAAGCC	AGAGAGAGGA	AGCAGTGT	GAATTAGTTA	ACATTCCAAC	TTTATTGAGA	GAACATGCTC
3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
TTTGCAAAACG	CAAATGTTA	GTTTGCTCTG	CAGAAAAGTT	CCTCAAGAAC	CCGTCAAAGC	TACAAGCTGG	ATTTGAGTAT	GTATACATAC	CAACTTTGTT
4010	4020	4030	4040	4050	4060	4070	4080	4090	4100
CTCCATTACA	TACTCACCCAC	GAATCTGAA	TTACCAAGTT	GCCAGACCTA	TCCTTAAGTT	CAGATCACGT	TTTGTGTATA	GCATTCCATT	GGAATTAAATT
4110	4120	4130	4140	4150	4160	4170	4180	4190	4200
CTGAGATTGTC	TATGCAAATC	TGAATCCCCC	TTAATGAAAT	CCTACAAATGC	AGACAAAACA	GGTCGGGGAT	GCCTTGCATC	AGTCTGGATC	CATGTATGTA
4210	4220	4230	4240	4250	4260	4270	4280	4290	4300
ACATTCTGAA	AAACAAAAGC	ATCAAGAAC	AAGGCAGAGA	ATCATATTTC	ATAGCCAAGT	GCATGAGCAT	GCAGCTGCAG	GTGTCCATTG	CAGATCTTG
4310	4320	4330	4340	4350	4360	4370	4380	4390	4400
GGGACCAACA	ATCATAATCA	AATCATGGG	TCACATCCCC	AAGACTGCAC	TTCCTTTTT	CAGCAAAGAT	GGGATTGCCT	GTCATCCATT	ACAAGATGTT
4410	4420	4430	4440	4450	4460	4470	4480	4490	4500
TCCCCCACTC	TGACAAAATC	ACTGTGCTCA	GTTGGATGTG	AGATAGAATC	TGCCAAGTTG	ATACTTCAG	AATCTGATCT	TAATGAGCTA	ATGGGCCACC
4510	4520	4530	4540	4550	4560	4570	4580	4590	4600
AGGACCTTAT	CACTGATAAG	ATTGCCATCA	GATCAGGTCA	ACGGACATT	GAGAGGTCCA	AATTCAAGCC	ATTAAAAAAA	TATGCAATCAA	TTCCAAACTT
4610	4620	4630	4640	4650	4660	4670	4680	4690	4700
GGAAGCCATC	AACTGAATGC	TCCAGCATCT	GAGAATAGAA	CCACAAATTAA	ATCATACTAT	TAGTAACAT	ACAATAAA	ACAATTTTAG	TCAACAGATT
4710	4720	4730	4740	4750	4760	4770	4780	4790	4800
ACCAAGATGT	TATCATAGGT	CCGAACTGAT	CAATCTAACAA	AAAAAAACTAA	ACGTTCCATA	ATAATCAAC	GTCAGGTCA	AAATACTCAA	CCATGCATCA
4810	4820	4830	4840	4850	4860	4870	4880	4890	4900
CCTACATCCA	ATGATAGTAT	GCATCTTTGT	TATGTACACT	GGAATTGTTAG	GTTCAAGGTG	CATTGCCGA	GACCAACTAC	TAAATATAGG	GGTCATTCAA
4910	4920	4930	4940	4950	4960	4970	4980	4990	5000
TCAAAGATAA	GATCACTCAT	GTACTATACT	GATGGTGGTG	CTAGCTTAT	TGTTGTTAAA	TTGCTACTTA	ATCTTCCCCC	AAGCAATGGA	ACATGCAACAA
5010	5020	5030	5040	5050	5060	5070	5080	5090	5100
TTACCACTCT	AGATGCATAC	AATGTTACCC	TATTTAAATT	ACTGACACCC	CTGATTGAGA	ACCTGAGCAA	AATCTCCGCT	GTTACAGATA	CCAAAACCCG
5110	5120	5130	5140	5150	5160	5170	5180	5190	5200
CCAAAGACGA	TTTGCAAGGAG	TCGTTGTTGG	ACTTGCTGCA	TTAGGAGTAG	CCACAGCTGC	ACAAATAACC	GCAGCTGTAG	CAATAGTTAA	AGCTAATGCA
5210	5220	5230	5240	5250	5260	5270	5280	5290	5300
AATGCTGCCG	CGATTAATAAA	TCTTGCATCT	TCAATTCAAT	CAACAAACAA	GGCAGTATCC	GATGTGATAG	ATGCATCAA	AAACATTGCA	ACTGCAGTTG
5310	5320	5330	5340	5350	5360	5370	5380	5390	5400
AAGCAATCCA	GGATCATATC	AATGGAGCTA	TTGTTAATGG	GATAACATCT	GCATCATGCC	GTGCCCATGA	TGCACTCATT	GGGTCAATAT	TAAATCTTTA
5410	5420	5430	5440	5450	5460	5470	5480	5490	5500
TCTCACTGAG	CTTACCAACAA	TATTCACAA	TCAAATAACA	AACCCCTGC	TGACACCCCT	CTCCATCCAA	GCTTTAAGAA	TTCTCCTCGG	TAGCACCTTG
5510	5520	5530	5540	5550	5560	5570	5580	5590	5600
CCAATTGTC	TTGAGTCCAA	ACTCAACACAA	AACCTCAACA	CAGCAGAGCT	GTCAGCTCC	GGACTGTTAA	CTGGTCAAAT	AATTCATT	TCCCCAATGTT
5610	5620	5630	5640	5650	5660	5670	5680	5690	5700
ACATGCAAAT	GCTAATTCAA	ATCAATGTT	CGACATTAT	AATGCAACCC	GGTGCAGAAG	TAATTGATCT	AATTGCTATC	TCTGCAAAC	ATAAATTGCA
5710	5720	5730	5740	5750	5760	5770	5780	5790	5800
AGAAGTAGTT	GTACAAAGTT	CGAATAGGAT	TCTAGAGTAT	GCAATGAAC	TACAAAATTA	TCCAGCCAAT	GACTGTTG	TGACACCGAA	CTCTGTATTC

FIGURE 10B

5810	5820	5830	5840	5850	5860	5870	5880	5890	5900
TGTAGATACA	ATGAGGGTTC	CCCTATCCCT	GAATCACAAAT	ACCAATGCTT	GAAGGGGAAT	CTTAATTCTT	GCACCTTTAC	CCCTATTATC	GGGAACCTTC
5910	5920	5930	5940	5950	5960	5970	5980	5990	6000
TTAAGCGATT	TGCATTTGCC	AATGGTGTGC	TCTATGCCA	CTGCAAATCT	TTGCTATGTA	AGTGTGCCGA	CCCTCCCCAT	GTGGTGTC	AAGATGATAC
6010	6020	6030	6040	6050	6060	6070	6080	6090	6100
CCAAGGCATC	AGCATAATTG	ATATTAAGAG	ATGCTCTGAG	ATGATGCTTG	ACACTTTCTC	ATTTAGGATC	ACATCTACGT	TCAATGCTAC	ATACGTGACA
6110	6120	6130	6140	6150	6160	6170	6180	6190	6200
GACTTCTCAA	TGATTAATG	AAATATTGTA	CATCTAACGTC	CTCTAGATT	GTCAAACCAA	ATCAATTCAA	TAAACAAATC	TCTTAAAAGT	GCTGAGGATT
6210	6220	6230	6240	6250	6260	6270	6280	6290	6300
GGATTGCA	TAGCAACTTC	TTTGCTAA	AAGCCAGGAC	AGCCAAGACA	CTTATTTCAT	TAAGTGAAT	AGCATTAA	CTATCAGTGA	TTACCTTGGT
6310	6320	6330	6340	6350	6360	6370	6380	6390	6400
TGTTGTGGGA	TTGCTGATTG	CCTACATCAT	CAAAGTAGTT	TCCCAAATCC	ATCAATTTCAG	AGCGCTAGCT	GCTACAAACAA	TGTTCCACAG	GGAAAATCCT
6410	6420	6430	6440	6450	6460	6470	6480	6490	6500
GCCTTCTTT	CCAAGAACAA	TCATGGAAAC	ATATATGGGA	TATCTTAAGA	AATCTATCAC	AAGTCCATAT	ATGTCCACAA	TTGATTCTTA	AGAACCAAAC
6510	6520	6530	6540	6550	6560	6570	6580	6590	6600
TCCAATGATT	ATCCTTTAA	CTTAAGTATA	ATAGTTAA	AATTAACATT	AAGCCTCCAG	ATACCAATGA	ATATGAATAT	ATCTCTAAGA	AAACCTGATT
6610	6620	6630	6640	6650	6660	6670	6680	6690	6700
ATTATGAT	AGTGTAGTAC	AATTAAGAA	AAAACCTAA	ATAACCACGA	ACCCCTAAGG	TGTCGTAACG	TCTCGTGACA	CTGGGTTCA	TTCAAAAATC
6710	6720	6730	6740	6750	6760	6770	6780	6790	6800
GACTTCTAA	CTAATTTAAC	ACCCATTCTT	ATATAAACAC	ACAGTATAAC	TTAATTACAA	AAGACCTAA	AAACTGACAC	AGCTTAATCC	ACTCACACATA
6810	6820	6830	6840	6850	6860	6870	6880	6890	6900
TAATTGTAAG	ATTAATAATA	ATGGAAGATT	ACAGCAATCT	ATCTCTTAA	TCAATTCTA	AAAGGACATG	TAGAATCATT	TTCCGAAC	CCACAAATTCT
6910	6920	6930	6940	6950	6960	6970	6980	6990	7000
TGGAAATATGC	ACATTGATTG	TTCTATGTT	AAGTATTCTT	CATGAAATAA	TTCATCTTGA	TGCTTCCTCT	GGTCTCATGA	ATTCTGATGA	TTCACAGCAA
7010	7020	7030	7040	7050	7060	7070	7080	7090	7100
GGCATTATTTC	AGCCTATTG	AGAACATTTA	AAATCATTGA	TTGCTTGGC	TAACCAAGATT	CTGTACAATG	TTGCAATAAT	AATTCTCTT	AAAATTGACA
7110	7120	7130	7140	7150	7160	7170	7180	7190	7200
GTATTGAGAC	CGTAATACTC	TCTGCTTYAA	AGGAYATGCA	TACTGGGAGC	ATGTCCAACA	CCAACGTGAC	ACCCGGAAAT	CTGCTTCTGC	ATGATGAGC
7210	7220	7230	7240	7250	7260	7270	7280	7290	7300
ATACATCAAT	GGAATAAACAA	AATTCTTGT	ACTTAAATCA	TACAATGGTA	CGCCTAAATA	TGGACCTCTC	CTAAATATT	CTAGCTTTAT	CCCCTCAGCA
7310	7320	7330	7340	7350	7360	7370	7380	7390	7400
ACATCTCCCC	ACGGGTGCAC	TAGAACATCA	TCATTTTCAC	TCAGTAAGAC	TCATTGGGT	TACACTCACA	ATGTAATACT	TGGAGATTGC	CTCGATTTC
7410	7420	7430	7440	7450	7460	7470	7480	7490	7500
CGACATCTAA	TCAGTATT	GCATGGGAA	TAATACAACA	ATCTGTCGA	GCATTTCCAA	TCTTCAGGAC	TATGAAAACC	ATTACCTAA	GTGATGGAA
7510	7520	7530	7540	7550	7560	7570	7580	7590	7600
CAATCGAAA	AGCTGTTAG	TCACTGCCAT	ACCAAGGAGT	TGTGCTTGT	ACTGCTATGT	AGCTACAAGA	TCTGAGAAAG	AAGATTATGC	CACAACTGAT
7610	7620	7630	7640	7650	7660	7670	7680	7690	7700
CTAGCTGA	TGAGACTTGC	TTTCTATTAT	TATAATGATA	CCCTTGTGAA	AAAGAGTCATA	TCTCTTCCAA	ATACAAACAGG	GCAATGGGCC	ACAATCAATC
7710	7720	7730	7740	7750	7760	7770	7780	7790	7800
CTGCAGTTGG	AAGCGGGATC	TATCATCTAG	GCTTTATTCTT	ATTCCCTGTA	TATGGTGGC	TCATAAAATGG	GACTCCTTCC	TACAACGAGC	AGTCCTCACG
7810	7820	7830	7840	7850	7860	7870	7880	7890	7900
CTATTTTATC	CCAACACATC	CCAACATAAC	CTGTGCCGA	AACTCCAGTG	AACGGGCTGC	AGCAGCACCG	GGTTCCATG	TCATCCGTTA	TCATTCAAAC
7910	7920	7930	7940	7950	7960	7970	7980	7990	8000
AGGTTGATTG	AGAGTGCTAT	TCTTATTGTC	CCATTATCTG	ACATGCAAAC	AGCAAGGTGT	GATCTAGTTA	TGTTAAACAA	TTCTCAAGTC	ATGATGGGT
8010	8020	8030	8040	8050	8060	8070	8080	8090	8100
CAGAAGGTAG	GCTCTATGTT	ATTGACAACA	ATTGTATTAA	TTATCAACGT	AGTCCCTCTT	GGTGGTCTGC	ATCGCTTTTC	TACAGGATCA	ATACAGATT
8110	8120	8130	8140	8150	8160	8170	8180	8190	8200
CTCTAAAGGA	ATTCCCTCTA	TCATTGAGGC	TCAATGGGT	CCGGCTTATC	AAGTTCCCG	CCCTGGAGTC	ATGCCATGTA	ATGCAACAAAG	TTTTGCGCT
8210	8220	8230	8240	8250	8260	8270	8280	8290	8300
GCTAATTGCA	TCACAGGAGT	GTATGCAAGAT	GTGTGGCCGC	TTAACGATCC	AGAACTCACA	TCACAAAATG	CTCTGAATCC	CAACTATCGA	TTTGCTGGAG
8310	8320	8330	8340	8350	8360	8370	8380	8390	8400
CCTTTCTAA	AAATGAGTCC	AACCGAACCA	ATCCCCACATT	TTACACTGCA	TCAGCCAAC	CCCTACTAAA	TACTACCGGA	TCAACAAACAA	CCAATCACAA
8410	8420	8430	8440	8450	8460	8470	8480	8490	8500
AGCAGCATAT	ACGCTCTCAA	CCTGCTTTAA	GAATACTGGA	ACTCAGAAGA	TTTATTGTTT	GATAATAATC	GAATGGGCT	CATCTCTTT	AGGGGAGTTC
8510	8520	8530	8540	8550	8560	8570	8580	8590	8600
CAAATAATAC	CATTCTAAAG	GGAACTATAA	CCTTAATACT	ATTGAATGAA	AACCTTAAGAT	TCAATAATAA	TTGAAAGGCT	CTCTATCTTA	TGTAATAGTT
8610	8620	8630	8640	8650	8660	8670	8680	8690	8700
ATACGTTTTG	GCTGTATTAG	AATGTTATAG	CATCTGCTG	TGTTCCCAT	ATGAAGCAAG	CCTTCAACAC	CGACTTAGGT	TCAATTCTT	CATCATTAC

FIGURE 10C

8710	8720	8730	8740	8750	8760	8770	8780	8790	8800
TGTTGTAATC	CAATCTTACT	AAAGTTATTG	TGATATTAA	AAAAAAATAA	CCTTTATATA	ATATAACAAT	ACTATTAAGA	TTATGATATA	GCCAGAATG
8810	8820	8830	8840	8850	8860	8870	8880	8890	8900
GCGGCCTCTT	CTGAGACT	CCTTCTGAA	GTCCACTGA	ACTCACCAAT	AGTCACAC	AAACTCATAT	ACTACTTATT	ACTAGGGCAC	TCCCCCATG
8910	8920	8930	8940	8950	8960	8970	8980	8990	9000
ATCTTGACAT	TTCTGAAATA	AGCCCTCTTC	ACAATAATGA	TTGGGATCAA	ATTGCCAGAG	AAGAATCAA	TCTTGCTGAA	CGACTTGGAG	TAGCTAAATC
9010	9020	9030	9040	9050	9060	9070	9080	9090	9100
TGAATTAAAT	AAACGTGTC	CCGCATTAG	AGCAACTAGA	GGCGTAGTC	ATGCAGCTGT	CCTTATATGG	CCTTCTTGTGAA	TACCAATTCT	TGTTAAATTC
9110	9120	9130	9140	9150	9160	9170	9180	9190	9200
CTACCTCATT	CTAACGTTCA	ACCAATAGAA	CAATGGTACA	AGTTGATCAA	TGCTTCATGT	AATACTATAT	CTGACTCAAT	TGATAGATGT	ATGGAGAATA
9210	9220	9230	9240	9250	9260	9270	9280	9290	9300
TTTCTATTAA	GCTTACTGGG	AAAAACAAATC	TATTCCTCG	ATCCAGAGGA	ACTGCAGGTG	CGAGTAAAAAA	CAGTAAATC	ACCCCTAACATG	ATATCCAATC
9310	9320	9330	9340	9350	9360	9370	9380	9390	9400
TATTTGGAA	TCAAACAACT	GGCACCCCTAA	TGTATCTTAA	TGGCTTACAA	TTAAATATCA	AATGCACAA	CTTATAATGC	ATCAAATTC	TCGTCAGCCG
9410	9420	9430	9440	9450	9460	9470	9480	9490	9500
ACTGATTTAG	TTCACATGTT	TGACACACGA	TCTGGCTTAA	TAGTTATCAC	CCCTGAACCT	GTATTGTTGTT	TTGATCGGTT	GAATAGTGT	TTAATGTATT
9510	9520	9530	9540	9550	9560	9570	9580	9590	9600
TTACATTTGA	GATGACTTTA	ATGGTAAGCG	ACATGTTGCA	GGGGAGGATG	AATGTCACGT	CTCTCTGCAC	TATTAGTCAT	TACTTATCTC	CACTAGGGCC
9610	9620	9630	9640	9650	9660	9670	9680	9690	9700
AAGGATCGAT	AGATTGTTT	CCATTGTTAGA	TGAATTAGCA	CAACTATTAG	GTGACACTGT	ATATAAAGTT	ATTGCATCTC	TTGAATCTTT	AGTATATGGG
9710	9720	9730	9740	9750	9760	9770	9780	9790	9800
TGTCTCACAA	TTAAAGATCC	AGTAGTGGAA	TTAGCAGGGT	CATTTCATTC	CTTTATTACA	CAAGAGATTA	TAGATATCCT	AATTGGTTCA	AAAGCCCTTG
9810	9820	9830	9840	9850	9860	9870	9880	9890	9900
ATAAGGATGA	ATCAATAACT	GTTACTACAC	AATTGTTAGA	TATATTTTCC	AACCTTTCTC	CAGATTTAAT	TGCTGAGATG	TTGTGTCCTA	TGAGACTTTG
9910	9920	9930	9940	9950	9960	9970	9980	9990	10000
GGGTCTACCT	ACTCTTACTG	CTGCGCAAGC	TGCGAGTAAA	GTGAGAGAAAT	CTATGTTGTC	AGGTAAGTTG	CTTGATTCTC	CTACAATAAT	GAAAACCTT
10010	10020	10030	10040	10050	10060	10070	10080	10090	10100
GCTTTTTTCC	ACACAATTTC	AATTAATGGT	TACCGTAGAA	AGAAAATGG	AATGTCGCCT	CCACTTATAC	TTCCCTAAAAA	TGCATCAAAA	AGCTTAATAG
10110	10120	10130	10140	10150	10160	10170	10180	10190	10200
AATTTCAACA	TGATAATGCT	GAATATCTT	ACGAATATAC	ACTCAAGCAT	TGAAAGAGA	TCTCTCTCAT	AGAATTTACA	AAAGTGTCTTG	ACTTTGATCC
10210	10220	10230	10240	10250	10260	10270	10280	10290	10300
TGGTGAGGAG	CTAACGATT	TTATGAAGGA	CAAGGCAATA	AGTGCTCCAA	AAAGTGTATTG	GATGAGTGT	TTTCGTAGAA	GTCTAATAAA	ACAAACGACAT
10310	10320	10330	10340	10350	10360	10370	10380	10390	10400
CAGAGACATC	ATATCCCTAT	GCCCCATCCA	TTAATAGAC	GTCTTAACT	CAATTTCTA	GAAGATGACA	GTTCGACCC	AGTTGCTGAG	CTCCAAATATG
10410	10420	10430	10440	10450	10460	10470	10480	10490	10500
TTACCACTGG	TGAATACCTC	CAAGATGACA	CATTGTTGTC	ATCTTACTCA	TTAAAGAGA	AAGAAATAAA	ACCAGATGGA	AGGATATTG	CTAACGTTAC
10510	10520	10530	10540	10550	10560	10570	10580	10590	10600
TAATAGAATG	CGGTCTGTG	AAAGTAAATGC	GGAGCAATT	CTTGCAAACT	ATGCAGGTAC	TCTAATGAG	AAAACGGAG	TTGTCTTGA	TCAATTATCA
10610	10620	10630	10640	10650	10660	10670	10680	10690	10700
CTGACCAAGT	CATTGCTTAC	TATGAGTCAA	ATTGGCATAA	TATCAGAAAA	GGCAAAAGAGA	TATACGCGAG	ATAACATCTC	ATCTCAAGGT	TTCCATACAA
10710	10720	10730	10740	10750	10760	10770	10780	10790	10800
TCAAGACTGA	CTCTAAAGAT	AAGAGGAAAA	GCAAAATCTG	ATCATCATAC	CTCACAGATC	CTGATGATAC	ATTGAACTT	AGTGCATGTT	TTATAACTAC
10810	10820	10830	10840	10850	10860	10870	10880	10890	10900
TGATCTTGT	AAATACTGTC	TTCAATGGG	ATATCAGACC	ATAATCCATT	TTGCTCGAAC	ATTAAACAGA	ATGTATGGG	TTCCACATT	ATTGAAATGG
10910	10920	10930	10940	10950	10960	10970	10980	10990	11000
ATTACATCTTC	GTTTAATTAG	GTCTACATTA	TATGTTGTTG	ATCCATTCAA	TCCCCCTGCT	GCGACTGATG	CTTTGCGATCT	AGATAAAGTA	TAAATGGTG
11010	11020	11030	11040	11050	11060	11070	11080	11090	11100
ATATCTTAT	AGTCTCTCCC	AAAGGAGGTA	TTGAAGGCCT	ATGTCAGAAA	ATGTGGACAA	TGATCTCTAT	TTCTGTGATC	ATCCCTCTCCT	CAGCCGAATC
11110	11120	11130	11140	11150	11160	11170	11180	11190	11200
CAAAACAAAGA	GTAATGAGCA	TGGTTCAAGG	AGATAATCAG	GCAATTGCGAG	TTACAACAG	AGTTCCCTAGA	TCATTAACCTA	GTATTCAAGAA	AAAGGAGTTA
11210	11220	11230	11240	11250	11260	11270	11280	11290	11300
GCCTATGCGAG	CAAGCAAGT	ATTTTTGAA	AGACTTGGG	CAAATAATTA	TGGGTTGGGT	CATCAGCTAA	AGGCTAGAA	AACTATAATA	AGTCCACAT
11310	11320	11330	11340	11350	11360	11370	11380	11390	11400
TCTTCATATA	TAGTAAACGG	GTATTTTATC	AAGGACGTAT	ACTAACACAG	GCACCAAA	ACGCTAGCAA	GCTATGTCCT	ACTGCGGATG	TATTAGGTGA
11410	11420	11430	11440	11450	11460	11470	11480	11490	11500
ATGTACTCAA	GCTTCTGTG	CAAATCTGTC	TACTACCAC	ATGAGATTAA	CAGAAAATGG	GGTTGAGAAA	GATACATGTT	ATAAGCTAA	TATTTATCAG
11510	11520	11530	11540	11550	11560	11570	11580	11590	11600
TCCATTGTC	AACTCACATA	TGATCTAATA	TTTCCCCAAT	ATTCCATACC	AGGTGAAACG	ATAAGTGGGA	TTTCTGTGCA	GCATCCAAGA	CTAATCTCAC

FIGURE 10D

11610	11620	11630	11640	11650	11660	11670	11680	11690	11700
GTATTGTTCT	GCTCCCTTCA	CAGCTAGGTG	GTCTTAATTA	CCTCGCATGC	AGCAGATTAT	TTAACCGCAA	TATCGGAGAT	CCTCTGGTA	CAGCTGTGGC
11710	11720	11730	11740	11750	11760	11770	11780	11790	11800
GGACCTCAAG	AGGTTAATTAA	AATGTGGTGC	TCTTGAATCA	TGGATACTGT	ACAATTACT	AGCAAGAAA	CCAGGGAAAG	GTTCATGGC	AACCTTAGCA
11810	11820	11830	11840	11850	11860	11870	11880	11890	11900
GCCGATCCGT	ACTCATGGAA	TCAAGAATAT	CTTTACCTC	CTACTACTAT	ACTTAAAGA	CATACTCAAC	ATACTTTAAT	GGAGATATGT	AGGAATCCTA
11910	11920	11930	11940	11950	11960	11970	11980	11990	12000
TGTTAAAGGG	AGTTTTCACA	GATAATGCAA	AAGAGGAGGA	AAATCCTCTT	GCAAAATTTC	TTCTTGATCG	TGATATAGTA	TTGCCAAGAG	TTGCGCACAT
12010	12020	12030	12040	12050	12060	12070	12080	12090	12100
TATAATAGAT	CAATCTAGCA	TCGGAAGGAA	GAAACAGATA	CAAGGATTTC	TTGACACCAC	AAGGACCAT	ATGAGACGT	CATTGAAAT	CAAACCACTC
12110	12120	12130	12140	12150	12160	12170	12180	12190	12200
TCAACTAAGA	AGACTCTTC	AGTTATAGAA	TATAATACAA	ATTACTTATC	TTATAACTAC	CCTGTACATAC	TTAACCTTT	ACCTATTCCC	GGATATTAA
12210	12220	12230	12240	12250	12260	12270	12280	12290	12300
ATTATATTAC	TGACCAAAC	TGCGAGTATTG	ATATATCTAG	AAAGTTAAGA	AAATTATCAT	GGTCTTCTTT	ATTGAATGGA	AGAACTTTAG	AAGGATTAGA
12310	12320	12330	12340	12350	12360	12370	12380	12390	12400
AACTCCAGAT	CCAATTGAAAG	TTGTCAATGG	TTCCTTGATT	GTAGGTACAG	GAGATTGTGA	TTTTGTATG	CAGGGTGATG	ACAAATTAC	TTGGTTCTTT
12410	12420	12430	12440	12450	12460	12470	12480	12490	12500
TTACCTATGG	GGATAATTAT	TGATGGAAT	CCTGAAACTA	ATCCACCCAT	CAGAGTCCA	TACATTGGGT	CTAGAACAGA	GGAAAGAAGA	GTTGCATCAA
12510	12520	12530	12540	12550	12560	12570	12580	12590	12600
TGGCATATAT	TAAAGGTGCC	ACACACAGTT	TGAAGGCTGC	TCTTAGGGGT	GCAGGGGTAT	ATATTGGGC	ATTGGGGAT	ACTATAGTGA	ACTGGAATGA
12610	12620	12630	12640	12650	12660	12670	12680	12690	12700
TGCACTTGAT	ATTGCAATA	CTAGAGTTAA	GATATCCCTA	GAGCAACTTC	AGACTCTCAC	ACCTCTTCC	ACATCTGCAA	ACATTACACA	CCGTTAGAT
12710	12720	12730	12740	12750	12760	12770	12780	12790	12800
GATGGAGCCA	CAACACTTAA	ATTCACCTCA	GCTAGTCCCT	ATGCATTTC	TAGTTTACT	CATATATCAA	ATGATCAACA	ATATTAGAA	ATAGATCAGA
12810	12820	12830	12840	12850	12860	12870	12880	12890	12900
GAGTAGTTGA	TTCCAATATT	ATTATTCAR	AAATTATGAT	AAACAGGACTT	GGGATTATG	AGACCTACCA	TAACCCACCT	ATAAGAACCT	CTACACAAGA
12910	12920	12930	12940	12950	12960	12970	12980	12990	13000
AATCACTCTC	CATTTGCACA	CTAGCTCATC	TTGTTGTGT	AGAAGTGTAG	ATGGCTGCCT	TATATGTGAA	AGCAATGGAG	AGGTTCCCCA	GATCACTGTT
13010	13020	13030	13040	13050	13060	13070	13080	13090	13100
CCCTATACTA	ATACATTGTT	ATATGATCCT	GACCCACTAG	CAGATTATGA	GATTGCACAT	CTAGATTACC	TCTCCTACCA	AGCTAAATT	GGAAGTACAG
13110	13120	13130	13140	13150	13160	13170	13180	13190	13200
ATTACTACTC	ACTCACTGAT	AAAATTGACC	TATAGCACA	TTAACATGCA	AAACAAATGA	TAACACTCAAT	AATTGGGTTA	GATGAAACAG	TATCGATTGT
13210	13220	13230	13240	13250	13260	13270	13280	13290	13300
CAATGATGCG	GTTATCCTAT	CTGACTATAC	TAAATCCTGG	ATTAGTGAAT	GTTCTTATAC	TAATAGAT	CTAGTTTTA	AATTATGGC	ATGGAATTTC
13310	13320	13330	13340	13350	13360	13370	13380	13390	13400
CTTCTTGAGC	TTGCATTCCA	GATGACTAC	TTAAGGATAT	CATCTTGGAC	AAATATATTT	GACTTACATT	ACATGACTTT	ACGCAGAATA	CCCGGAAC
13410	13420	13430	13440	13450	13460	13470	13480	13490	13500
CTCTAAATAA	TATTGCACT	ACTATTAGCC	ATCCAAATT	ACTGAGACGT	GCAATGAATC	TTGATATTAT	CACTCCTATA	CATCACCGT	ATCTAGCTTC
13510	13520	13530	13540	13550	13560	13570	13580	13590	13600
ATTAGATTAT	GTCAAATTAA	GTATTGATGC	AATTCACTGG	GGAGTTAAAC	AAGTTCTTGC	TGATTTATCA	AATGGAATTG	ATCTTGAAT	CTTGATTCTT
13610	13620	13630	13640	13650	13660	13670	13680	13690	13700
TCAGAGGATT	CAATGGAAT	TAGTGATAGG	GCAATGAATC	TCATTGCTAG	AAAACTAAT	CTCCTTGCAC	TTGTTAAAGG	TGAGAACTAC	ACTTTTCCAA
13710	13720	13730	13740	13750	13760	13770	13780	13790	13800
AAATTAAAGG	GATGCCACCA	GAAGAAAAGT	GTTTAGTCTT	AACTGAATAT	CTAGCAATGT	GTATCAAAA	TACTCACCAC	TTAGATCCAG	ATCTTCAAA
13810	13820	13830	13840	13850	13860	13870	13880	13890	13900
GTATTTATAT	AATCTAACTA	ATCCAAATT	GACCGCATT	CCCAGTAACA	ACTTCTACTT	AACTAGGAAA	ATCCTCAATC	AAATTAGAGA	ATCAGACGAA
13910	13920	13930	13940	13950	13960	13970	13980	13990	14000
GGACAAATATA	TTATCACCTC	ATATTATGAA	TCCTTCGAAC	AATTAGAAAC	AGATATAATT	CTTCATCTCA	CTTAACTGCA	TCCTTATGAT	AATTCAGAAA
14010	14020	14030	14040	14050	14060	14070	14080	14090	14100
CTCTAACAAA	GTTTGATTAA	TCCCTTGACA	TCTTCCACA	TCCAGAATCT	CTCGAGAAAT	ATCCTCTTCC	AGTTGATCAT	GACTCTCAAT	CTGCAATTTC
14110	14120	14130	14140	14150	14160	14170	14180	14190	14200
AACACTAAATT	CCAGGCCCTC	CTTCTCATCA	TGTATTACGA	CCACTGGGG	TGTCCTCTAC	AGCTTGGTAT	AAAGGGATAA	GTTATTGTTAG	GTATCTAGAA
14210	14220	14230	14240	14250	14260	14270	14280	14290	14300
ACACAAAAGA	TACAGACTGG	TGATCATCTT	TATTTAGCTG	AAGGAAGCGG	CGCTTCAATG	TCACCTCTAG	AACCTCTATT	TCCAGGAGAT	ACTGCTTATT
14310	14320	14330	14340	14350	14360	14370	14380	14390	14400
ATAATAGTCT	TTTTAGTAGT	GGAGAGAATC	CTCCACAGAG	AAACTACGCC	CCTCTTCCAA	CTCAATTGTT	ACAGAGTGT	CCATATAAT	TGTGGCAAGC
14410	14420	14430	14440	14450	14460	14470	14480	14490	14500
TGATCTTGCT	GATGATAGCA	ACTTGATAAA	AGATTTGTC	CCATTATGGA	ATGGAAATGG	TGCAGTACAA	GACTTATCAA	CAAAGGATGC	AGTTGCATT

FIGURE 10E

14510	14520	14530	14540	14550	14560	14570	14580	14590	14600
ATAATACATA	AAGTAGGAGC	AGAAAAAGCA	TCTCTTGTCC	ATATAGATCT	CGAATCGACT	GCTAATATAA	ATCAGCAAAC	TCTGTCCAGA	TCCCAGATT
14610	14620	14630	14640	14650	14660	14670	14680	14690	14700
ATTCATTAAT	TATAGCAACT	ACTGTTCTTA	AGAGGGGTGG	GATATTAAATT	TATAAGACAT	CATGGCTTCC	TTTTCTAGA	TTTAGTCAAC	TAGCAAGCCT
14710	14720	14730	14740	14750	14760	14770	14780	14790	14800
TCTTTGGTGC	TTTTTGACC	GGATCCATCT	AATACTAGT	AGCTATTCTG	ATCCTCACAG	TCATGAGGTT	TATCTGTAT	GTAGACTTGC	CGCAGATT
14810	14820	14830	14840	14850	14860	14870	14880	14890	14900
AGAACTATCG	GTTCAGTGC	AGCTCTAGTA	ACTGCTACTA	CTCTTCACAA	TGACGGATTC	ACAACAATAC	ATCCTGATGT	TGTTTGATGT	TATTGGCAC
14910	14920	14930	14940	14950	14960	14970	14980	14990	15000
ACCATCTTGA	AAATGTTGGG	AGAGTCGGAA	AAGTAATTGA	TGAGATACTT	GATGGTTAG	CCACCAACTT	CTTGCAGGA	GATAATGGAC	TTATTCTAAC
15010	15020	15030	15040	15050	15060	15070	15080	15090	15100
ATGTGGAGGA	ACTCCCAGCT	CCAGAAAATG	GTTGGAGATT	GACCAGTTAG	CATCATTTGA	TTGGTTCAA	GATGCTCTGG	TGACACTTAT	CACTATACAC
15110	15120	15130	15140	15150	15160	15170	15180	15190	15200
CTAAAGGAAA	TTATAGAACT	GCAATCATCA	CATACAGAAAG	ATTATACATC	TCTCCCTTTC	ACACCTTATA	ATATTGGTCC	AGCAGGGAAA	GTTAGAACT
15210	15220	15230	15240	15250	15260	15270	15280	15290	15300
TCATCAAATT	AATTCTAGAA	CGATCTTAA	TGTATACAGT	CCGAAATTGG	TTAGTGTAC	CCAGTTCCAT	CCGGGATTCT	GTACGACAAG	ATTGGAAAT
15310	15320	15330	15340	15350	15360	15370	15380	15390	15400
AGGGTCATTT	AGATTAATGT	CTATTTTAAG	TGAACAGACA	TTTCTTAAAG	AGACACCCAC	AAAAAAATAC	TTACTTGATC	AGCTTACAAG	GACATATATA
15410	15420	15430	15440	15450	15460	15470	15480	15490	15500
TCAACCTTCT	TTAACTCTCA	CTCAGTCCTT	CCTCTTCACC	GTCCATATCA	AAAACAATAA	TGGAAAGCCT	TAGGTAGTGT	AATATATTGT	TCGGAGACAG
15510	15520	15530	15540	15550	15560	15570	15580	15590	15600
TTGATATACC	TCTAATTAAA	GACATTGAGA	TAGAAGATAT	TAATGATTT	GAGGATATCG	AGAGGGTAT	CGATGGCGAA	GAATTATGAC	AAACATGATT
15610	15620	15630	15640	15650					
ATAAGAACTC	ATGATAGTTT	TATTTAAGAA	AAACATATTG	ATTTTCCCCCT	TGGT				

Human Parainfluenza Virus Type 2 Strain Greer antigenomic sense cDNA Sequence Range: 1 to 15654

10	20	30	40	50	60	70	80	90	100
ACCAAGGGGA	GAATCAGATG	GCATCGTTAT	ATGACGAATT	GCAAAAAGAT	TACGTAGGTC	CGGAACCACT	AGATTCCGGT	GCCGGTAACG	ATTCCAGTT
110	120	130	140	150	160	170	180	190	200
TATACTATCT	GATCATTCCTC	TATCTCTATT	AAGGATATT	CTAGTCTAAA	GTTCAAAATG	TCAAGTGT	TAAAGACATT	TGAAAGATT	ACTATACAAC
210	220	230	240	250	260	270	280	290	300
AGGAGCTTCA	GGAGCAATCT	GATGACACTC	CAGTACCTCT	TGAGACAATC	AAACCTACAA	TCAGGGTATT	TGTCATCAAT	AATAATGATC	CTGTCGTAAG
310	320	330	340	350	360	370	380	390	400
ATCTAGACTT	TTATTCITTA	ATCTACGAAT	CATTATGAGT	AACACTGCAA	GAGAGGGACA	TAGAGCTGGT	GCTCTCCCTA	GTCTTTATC	ACTACCTCT
410	420	430	440	450	460	470	480	490	500
GCAGCTATGA	GTAATCACAT	CAAATTAGCC	ATGCATTAC	CAGAAGCCAG	CATAGATAGA	GTAGAGATAA	CAGGGTTG	GAATAATTCA	TTCCGAGTC
510	520	530	540	550	560	570	580	590	600
TTCCAGATGC	TCGATCAACT	ATGTCAGAG	GAGAGGTGCT	GGCTTTGAA	GCATTAGCTG	AGGACATTCC	TGATACCCT	AATCACCAA	CTCCATTG
610	620	630	640	650	660	670	680	690	700
AAATAATGAT	GTAGAAAGATG	ACATATTGAA	TGAAACAGAG	AAATTCTTAG	ATGTTTGCTA	CAGTGTGTT	ATGCAGGCAT	GGATAGTAAC	ATGCAAGTGT
710	720	730	740	750	760	770	780	790	800
ATGACTGCTC	CTGATCAACC	ACCACTATCA	GTAGCAAAGC	GGATGGCTAA	ATATCAACAA	CAAGGGAGAA	TCAATGCTAG	GTATGTACTA	CAACCTGAAG
810	820	830	840	850	860	870	880	890	900
CACAAAGACT	AATTCAAAAT	GCCATCCGCA	AGTCAATGGT	AGTAAGGCAT	TTCATGACTT	ATGAGCTCA	ACTTTCACAA	TCAAGATCTT	TGCTAGCAAA
910	920	930	940	950	960	970	980	990	1000
CCGCTACTAT	GCTATGGTGG	GAGACATTG	CAAGTACATT	GAACACAGCG	GAATGGGAGG	ATTTTCTTA	ACACTTAAAT	ATGGACTTGG	AACAAGATGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
CCTACATTGG	CTCTTGCAGC	ATTTCTGGG	GAACCTCAGA	AATTAAAAGC	TCTCATGCTA	CATTATCAGA	GTCTAGGACC	CATGGCCAAG	TACATGGCTC
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TATTAGAAC	ACCAAAACTG	ATGGATTTTG	TCCCATCTGA	ATATCCATT	GTTTATAGCT	ATGCAATGGG	TATGGAACT	GTCCCTTGATA	CAAATATGAG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AAATTATGCA	TACGGTAGAT	CATATTTAA	TCCGCAATAT	TTTCAGCTAG	GAGTAGAAC	AGCAAGGAAA	CAGCAGGGAG	CTGTTGACAA	CAGGACAGCA
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
GAGGACCTCG	GCATGACTGC	TGCAAGACAA	GCAGACCTCA	CTGCAACCAT	ATCAAAAGCTA	TCCTTGTC	AATTACCTAG	GGGTAGACAA	CCAATATCTG
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ACCCATTTC	TGGAGCAAAT	GACAGAGAAA	TGGGAGGACA	AGCAAATGAT	ACACCTGT	ATAACTTCAA	TCCAATCAAT	ACTCGGAGGT	ATGACAACTA
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
TGACAGTGAT	GGTGGAGACA	GAATTGACAA	CGATCAAGAT	CAAGCTATCA	GAGAGAATAG	AGGAGAGCCT	GGACAACCAA	ACAACCGAG	AAAGTGACAA
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
CAGCAGAGAT	TCAACCCCCC	CATACCGAA	AGAACATCG	GTATGAGCAG	TGAAGAGTTC	CAACATTCAA	TGAATCAGTA	CATCCGTGCT	ATGCATGAGC
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
AATAACAGAG	CTCCCAGGAT	GATGATGCCA	ATGATGCCAC	AGATGGGAAT	GACATTCTC	TTGAGCTAGT	TGGAGATT	GATTCCTAAC	TCTCAATGTC
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
ATACAACCG	ATATACACAT	CCACATCACT	CAGAGATACA	GCTGCCACTC	ACACACTCAT	CCAGACAAAT	CAAACATGAC	TCACATCATT	CGGAAACAAAT
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
TCTCTATAA	TTAAGAAAAA	AATCATAGGC	CCGGACGGGT	TAGAAATCCG	GTGCTTGTC	GTGATCAGAT	AACCTCCACA	CCAGAACAT	ACAATCATGG
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
CCGAGGAACC	AACATACACC	ACTGAGCAAG	TTGATGAATT	AATCCATGCT	GGACTGGAA	CAGTAGATT	CTTCCTATCT	AGACCCATAG	ATGCTCAGTC
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TTCTTTAGGC	AAAGGCAGCA	TCCCACCAAG	TGTCACAGCT	GTTCTAACTA	GTGCAGCGGA	GGCAAATCC	AAACCACTTG	CTGCTGGTCC	AGTTAAACCC
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
AGGCGGAAGA	AAGTGATCG	CAATACTACT	CCATACACTA	TTGCAGACAA	TATTCCACCT	GAGAAGCTAC	CGATCAACAC	TCCAATACCC	AATCCATTAC
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
TTCCACTGGC	ACGCCCTCAC	GGAAAGATGA	CAGACATTGA	CATTGTC	GGGAACATTA	CAGAAGGATC	GTACAAAGGT	GTGGAGCTG	CTAAATTAGG
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
GAAGCAGACA	CTACTCACAA	GGTTCACCTC	GAATGAGCCA	GTCTCC	GGGAACATGC	CCAAAGACCCC	AACTTTAAGA	GGGGGGGAGC	TAATAGAGAA
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
AGAGCAAGAG	GCAACCATGAG	GAGAGAATGG	AGTATTGCA	GGGTC	GGAGTCAAA	GTCTTCGAGT	GGTGTAA	CAGGTGTGCC	CCAGTCACGG
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
CCTCAGCTCG	CAAGTTCACC	TGCAATGCG	GATCCTGCC	CAGCATCTGC	GGAGAATGTG	AAGGAGATCA	TTGAGCTCTT	AAAGGGACTT	GATCTTCGCC
2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
TTCAGACTGT	AGAAGGGAAA	GTAGATAAAA	TTCTTGC	AACTCT	ATAATCAATC	TTAAAAATGA	AATGACTAGT	CTCAAGGC	GTGTTGCAAC
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
TGTGGAAGGT	ATGATAACAA	CAATTAAAT	CATGGATCCC	AGTACACCAA	CTAATGTCCC	TGTAGAGGAG	ATCAGAAAGA	GTTTACACAA	TGTTCCAGTA

FIGURE 11A

2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
GTAATTGCCG	GTCCTAATAG	TGGAGGCTTC	ACAGCCGA	GCAGTGATAT	GATTTCAATG	GATGAAC	CTAGACCTAC	ACTCTCATCA	ACAAAAAGGA
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
TCACACGAAA	GCCTGAATCC	AAGAAAGATT	TAACAGGCA	AAAACAACT	TTGATGCAGC	TTGCAAATGA	CTGCATCTCG	CCTCCAGATA	CCAAGACTGA
3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
GTTCTGACT	AAGATTCAAGG	CAGCAACCAC	AGAACATCACAG	CTTAACGAAA	TTAACCGTC	AATAATACGC	TCTGCAATAT	AAAATGAGGT	GCAGTCACAC
3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
AAGAGACACT	CAACATGCAT	CCAATCAAGA	TCCGACTTC	ATCCATCCAA	AAACACGCC	ACAATTGTC	ACACCAAGAA	ACACCCACAG	CCGAACCATG
3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
CTCAACCAAA	AGACCCAAAC	AAACACCTAC	ATCAATAGAA	GGCTGGACAT	GATAAATTAA	ATAAAAAAAG	AAAAGAAGTT	AAGTAAAATT	TAAAGGACAC
3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
AATAGAGAAA	ATCTAGGTCC	GAAAGCTTGC	CTCTCAGACA	GATCCCCAA	TCATAGTCA	AAACCCAAAC	ACAGCAGCAG	ACATGCTTAT	AATATCATT
3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
CCAGCAGATC	CAACTTCACC	CAGTCATACC	CTTACTCCGT	TTCCAATACA	ACTTGACACC	AAAGATGGCA	AGGCAGGGAA	ACTCCTTAA	CAGATTGCA
3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
TTAGGTATCT	AAATGAGCCT	ATTCTCGCC	ATACACCAAT	AACTTCATC	AATACGTATG	GATTGTTA	TGCTCGAGAC	ACTTCAGGG	GCATTCAAG
3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
TGAGATCAGC	AGTGCACCTAG	CTGCAGGGTC	CATAACAGCA	TGCATGATGA	CGCTAGGTCC	TGGTCCAAT	ATTCAAGATG	CAAATCTAGT	GCTAAGATCT
3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
CTGAATGAAT	TCTACGTAAA	AGTCAAGAAG	ACATCAAGCC	AGAGAGAGGA	AGCAGTGT	GAATTAGTTA	ACATTCCAAC	TTTATTGAGA	GAACATGCTC
3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
TTTGCAACG	CAAATGTTA	GTATGCTCG	CAGAAAAATT	CCTCAAGAAC	CCGTCAAAGC	TACAAGCTGG	ATTTGAGTAT	GTATACATAC	CAAACCTTTG
4010	4020	4030	4040	4050	4060	4070	4080	4090	4100
CTCCATTACA	TACTCACCA	GAAATCTGAA	TTACCAAGTT	GCCAGACCTA	TCCTTAAGTT	CAGATCACGC	TTTGTGTATA	GCATTCAATT	GGAATTAATC
4110	4120	4130	4140	4150	4160	4170	4180	4190	4200
CTGAGATTGC	TATGCAAATC	TGACTCCCC	TTGATGAAAT	CCTACAAATGC	AGACAGAAC	GGTCGGGGAT	GCCTCGCATC	AGTCTGGATC	CTTGTATGTA
4210	4220	4230	4240	4250	4260	4270	4280	4290	4300
ACATTCTGAA	AAACAAAAGC	ATCAAGAAC	AAGGCAGAGA	ATCATATTTC	ATAGCTAAAGT	GCATGAGCAT	GCAGCTGCAG	GTGTCATTG	CAGATCTTG
4310	4320	4330	4340	4350	4360	4370	4380	4390	4400
GGGACCAACA	ATCATAATCA	AATCATTTGGG	TCACATCCCC	AAAGACTGCAC	TTCCCTTTTT	CAGCAAAGAT	GGGATTGCCT	GTCATCCATT	ACAAGATGTT
4410	4420	4430	4440	4450	4460	4470	4480	4490	4500
TCCCCTAAATC	TGACAAAATC	ACTGTGGCA	GTTGGATGTG	AGATAGAACT	TGCCAAGTTG	ATACTTCAAG	AATCTGATCT	TAATGAGCTA	ATGGGCCACC
4510	4520	4530	4540	4550	4560	4570	4580	4590	4600
AGGACCTTAT	CACTGATAAG	ATTGCCATT	GATCAGGTCA	ACGGACATT	GAGAGGTCCA	AATTCAAGCC	ATTCAAAAAAA	TATGCATCAA	TTCCAACATT
4610	4620	4630	4640	4650	4660	4670	4680	4690	4700
GGAAGCCATC	AACTGAATGC	TCCAGCATCT	GAGAATAGAA	CCACAAATCA	GTCATACTAC	TAGTCACATT	ACAATAATCA	ACAATTTTAG	TCAACTGATT
4710	4720	4730	4740	4750	4760	4770	4780	4790	4800
ACCAAGATGT	TATCATAGGT	CCGAACTGAT	CAATCTAAC	AAAAAAACTAA	ACGTTCCACAA	ATAATCAAC	GTTCAGGCCA	AAATATTTCAG	CCATGCATCA
4810	4820	4830	4840	4850	4860	4870	4880	4890	4900
CCTGCATCCA	ATGATAGTAT	GCATCTTGT	TATGTACACT	GGAATTGTTAG	GTTCAAGATGC	CATTGCTGGA	GATCAACTAC	TTAATATAGG	GGTCATTCAA
4910	4920	4930	4940	4950	4960	4970	4980	4990	5000
TCAAAGATAA	GATCACTCAT	GTACTTACT	GATGGTGGTG	CTAGCTTTAT	TGTTGTTAAA	TTGCTACCTA	ATCTTCCCC	AAGCAATGGA	ACATGCAACA
5010	5020	5030	5040	5050	5060	5070	5080	5090	5100
TCACCAAGTCT	AGATGCATAT	AATGTTACCC	TATTTAAGTT	ACTAACACCC	CTGATTGAGA	ACCTGAGTAA	AATTTCACCT	GTACAGATA	CCAAAACCCG
5110	5120	5130	5140	5150	5160	5170	5180	5190	5200
CCAAGAACGA	TTTGCAAGGAG	TAGTTGTTGG	ACTTGCTGCA	TTAGGAGTAG	CCACAGCGC	ACAAATAACT	GCAGCTGTAG	CAATAGTGAA	AGCTAATGCA
5210	5220	5230	5240	5250	5260	5270	5280	5290	5300
AATGCTGCTG	CGATAAAACAA	TCTTGCATCT	TCACATTCAAT	CCACCAACAA	GGCAGTATCC	GATGTGATAG	ATGCATCAAG	AAACATTGCA	ACCGCAGTTC
5310	5320	5330	5340	5350	5360	5370	5380	5390	5400
AAGCAATTCA	GGATCACATC	AATGGAGCTA	TGTTAATGG	GATAACATCT	GCATCATGCC	GTGCCCCATGA	TGCACCTATT	GGGTCATAT	TAAATCTTAA
5410	5420	5430	5440	5450	5460	5470	5480	5490	5500
TCTCACTGAG	CTTACCAACAA	TATTTCATAA	TCAAATAACA	AACCCCTGGCC	TGACACCAC	CTCCATCAA	GCTTTAAGAA	TCCTCCTCGG	TAGCACCTTG
5510	5520	5530	5540	5550	5560	5570	5580	5590	5600
CCAATTGTCA	TTGAGTCCAA	ACTCAACACA	AACCTCAAC	CAGCAGAGCT	GCTCAGTTCC	GGACTGTTAA	CTGGTCAAAT	AATTTCACATT	TCCCCAATGT
5610	5620	5630	5640	5650	5660	5670	5680	5690	5700
ACATGC	AAAT	GCTAATTC	ATCAATGTT	CGACATT	AATGCAACCC	GGTGCAGAAG	TAATTGATCT	AATTGCTATC	TCCGAAACCA
5710	5720	5730	5740	5750	5760	5770	5780	5790	5800
AGAAGTGGTT	GTACAAGTTC	CGAATAGGAT	TCTAGAGTAT	GCAAAATGAAC	TACAAAATT	CCCAGCCAAT	GACTGTGTCG	TGACACCGAA	CTCTGTATTT

FIGURE 11B

5810	5820	5830	5840	5850	5860	5870	5880	5890	5900
TGTAGATACA	ATGAGGGTTC	CCCTATCCCT	GAATCACAAAT	ATCAATGCTT	GAGGGGAAT	CTTAATTCTT	GCACCTTTAC	CCCTATTATC	GGGAACCTTC
5910	5920	5930	5940	5950	5960	5970	5980	5990	6000
TTAAGCGATT	CGCATTGCT	AATGGTGTGC	TCTATGCCA	CTGCAAATCT	TTGCTATGTA	GGTGTGCCGA	CCCCCCCCTA	GTTGTATCCC	AGGATGATAAC
6010	6020	6030	6040	6050	6060	6070	6080	6090	6100
CCAAGGCATC	AGCATAATTG	ATATTAAGAG	ATGCTCTGAG	ATGATGCTTG	ACACTTTTC	ATTAGGATC	ACATCTACTT	TCAATGCTAC	GTACGTGACA
6110	6120	6130	6140	6150	6160	6170	6180	6190	6200
GACTTCTCAA	TGATTAATGC	AAATATTGTA	CATCTAACGTC	CTCTAGATT	GTCAAATCAA	ATCAATTCAA	TAACAAATC	TCTTAAAAGT	GCTGAGGATT
6210	6220	6230	6240	6250	6260	6270	6280	6290	6300
GGATTGCAGA	TAGCAACTTC	TTTGCTAATC	AAGCCAGGAC	AGCCAAGACA	CTTTATTAC	TAAGTGAAT	AGCATTAAATA	CTATCAGTGA	TTACTTTGGT
6310	6320	6330	6340	6350	6360	6370	6380	6390	6400
TGTCGTGGGA	TTGCTGATTG	CCTACATCAT	CAAGCTGGTT	TCTCAAATCC	ATCAATTCA	ATCGCTAGCT	GCTACAAACAA	TGTTCCACAG	GGAAAATCCT
6410	6420	6430	6440	6450	6460	6470	6480	6490	6500
GCCTTCTTT	CCAAGAAATAA	CCATGGAAAC	ATATATGGGA	TATCTTAAGA	AATCTATCAC	AAAGTCTATAT	ATGTCCACAA	TTGACCCCTA	AGAACCAAAC
6510	6520	6530	6540	6550	6560	6570	6580	6590	6600
TCCAACGATT	ATCCGTTAAA	TTTAAGTATA	ATAGTTAAA	AATTAACATT	AAGCCTCCAG	ATACCAATGA	ATATGAATAT	ATCTCTTAGA	AAACCTGATT
6610	6620	6630	6640	6650	6660	6670	6680	6690	6700
ATTATGTGAT	ACCGTAGTAC	AATTTAAGAA	AAAACCTAAA	ATAAGCACGA	ACCCCTTAAGG	TGTCGTAACG	TCTCGTGACA	CCGGGTTCA	TTCAAAATATC
6710	6720	6730	6740	6750	6760	6770	6780	6790	6800
GACCTCTAAC	CCAATTTAAC	ACCCATTCTT	ATATAAGAAC	ACAGTATAAT	TTAACATCAA	AAAGCCTCAA	AAACTGACAC	AGCTTGATCC	ACTCAACATA
6810	6820	6830	6840	6850	6860	6870	6880	6890	6900
TAATTGTAAG	ATTAATAAT	ATGGAAGATT	ACAGCAATCT	ATCTCTTAA	TCAATTCC	AAAGGACATG	TAGAATCATT	TTCCGAACTG	CCACAATTCT
6910	6920	6930	6940	6950	6960	6970	6980	6990	7000
TGGAATATGC	ACATTGATTG	TTCTATGTT	AAAGTATTCT	CATGAGATAA	TTCATCTTGA	TGTTCCCTCT	GGTCTCATGG	ATTCCGATGA	TTCACAGCAA
7010	7020	7030	7040	7050	7060	7070	7080	7090	7100
GGCATTATTC	AGCCTATTAT	AGAATCATTAA	AAATCATTAA	TTGCTTTGGC	TAACCAGATT	CTGTACAATG	TTGCAATAAT	AATTCCCTCT	AAAATTGACA
7110	7120	7130	7140	7150	7160	7170	7180	7190	7200
GTATCGAGAC	TGTAATATAC	TCTGCTTTAA	AGGATATGCA	TACTGGAGC	ATGTCAAACA	CCAACTGTAC	ACCCGGAAAT	CTGCTTCTGC	ATGATGCCAGC
7210	7220	7230	7240	7250	7260	7270	7280	7290	7300
GTACATCAAT	GGAATAAAACA	AAATCCTTGT	ACTTAAATCA	TACAATGGGA	CGCCTAAATA	TGGACCTCTC	CTAAATATT	CCAGCTTTAT	CCCCTCAGCA
7310	7320	7330	7340	7350	7360	7370	7380	7390	7400
ACATCTCCC	ACGGGTGCAC	TAGAATACCA	TCATTTTCAC	TCATTAAGAC	CCATTGGTGT	TACACTCACA	ATGTAATACT	TGGAGATTGC	CTCGATTTC
7410	7420	7430	7440	7450	7460	7470	7480	7490	7500
CGACATCTAA	TCAGTATTTA	GCAATGGGG	TAATACAACA	ATCTGCTGA	GCATTTCAA	TCTTCAGGAC	TATGAAAACC	ATTTACCTAA	GTGATGGAAAT
7510	7520	7530	7540	7550	7560	7570	7580	7590	7600
CAATCGAAA	AGCTGTTCA	TCACTGCTAT	ACCAGGAGGT	TGTCGTTGT	ATTGCTATGT	AGCTACAAAGA	TCTGAGAAAG	AAGATTATGC	CACAACTGAT
7610	7620	7630	7640	7650	7660	7670	7680	7690	7700
CTAGCTGAA	TGAGACTTGC	TTTCTATTAT	TATAATGATA	CTTTTATTGA	AAGAGTCATA	TCTCTTCAA	ATACAAACAGG	GCAATGGGCC	ACAATCAATC
7710	7720	7730	7740	7750	7760	7770	7780	7790	7800
CTGCAGTTGG	AAGCGGGATC	TATCATCTAG	GCTTTATT	ATTTCCTGT	TATGGTGGTC	TCATAAAGGG	GACTCCTTCC	TACAACAAGC	AGTCCTCACG
7810	7820	7830	7840	7850	7860	7870	7880	7890	7900
CTATTTTATC	CCAAAACATC	CCAAACATAAC	CTGTGCCGGT	AAATCCAGCG	AAACAGGCTGC	AGCAGCACGG	AGTTCCATATG	TAATCCGTTA	TCACTCAAAC
7910	7920	7930	7940	7950	7960	7970	7980	7990	8000
AGGTGATTG	AGAGTGCTGT	TCTTATTGTC	CCATTGCTG	ACATGCACAC	AGCAAGGTGT	AATCTACTTA	TGTTAAACAA	TTCTCAAGTC	ATGATGGGT
8010	8020	8030	8040	8050	8060	8070	8080	8090	8100
CAGAAGGTAG	GCTCTATGTT	ATTGACAATA	ATTGTATT	TTATCACACG	AGTTCCCTTT	GGTGGGCTGC	ATCGTTTTT	TACAGGATCA	ATACAGATT
8110	8120	8130	8140	8150	8160	8170	8180	8190	8200
TTCTAAAGGA	ATTCTCTCTA	TCATTGGGC	TCAATGGGA	CCGTCCTATC	AAAGTCCCCCG	TCCTGGAGTC	ATGCCATGCA	ATGCAACAAG	TTTTGCCCC
8210	8220	8230	8240	8250	8260	8270	8280	8290	8300
GCTAATTGCA	TCACGGGGT	GTACCGAGAT	GTGCGCCGC	TTAACGATCC	AGAACCCACA	TCACAAAATG	CTCTGAATCC	CAACTATCGA	TTTGCTGGAG
8310	8320	8330	8340	8350	8360	8370	8380	8390	8400
CCTTCTCTAG	AAATGAGTCC	AACCGAACCA	ATCCCACATT	CTACACTGCA	TCAGCCAGCG	CCCTACTAAA	TACTACCGGA	TCAACAAACA	CCAATCACAA
8410	8420	8430	8440	8450	8460	8470	8480	8490	8500
AGCAGCATAT	ACGCTCTCAA	CCTGCTTTAA	GAATACTGGA	ACTCAAAGA	TTTATTGTTT	GATAATAAT	GAAATGGGCT	CATCTCTTT	AGGGGAGTTC
8510	8520	8530	8540	8550	8560	8570	8580	8590	8600
CAAATAATAC	CATTCTAAG	GGAACTAATA	CCTTAATACT	ATTGAATGAA	GACTCCAGAT	TCAATAATAA	TTGAAAGGCT	CTCTATCTTA	TGCAATAGTT
8610	8620	8630	8640	8650	8660	8670	8680	8690	8700
ATACGTTTTG	GCTGATTAG	AATGTTATAG	CATTCTGCTG	TTTTCCCAT	ATGAAGCAAT	CCTCAACAC	CGACTTAGGT	TCAATTTCT	CATCATTTAC

FIGURE 11C

8710	8720	8730	8740	8750	8760	8770	8780	8790	8800
TGTTGTAATT	CAATCTTACT	AAAGTTTATC	CGATATTAA	GAAAAAATAA	CCTTTATATA	ATGTAACAAT	ACTATTAAAGA	TTATGATATA	GGCCAGAAATG
8810	8820	8830	8840	8850	8860	8870	8880	8890	8900
GCGGCCTCTT	CTGAGATACT	CCTTCCTGAA	GTCCACTTGA	ACTCACCAAT	AGTCACAC	AAACTCATAT	ACTACTATT	ACTAGGGCAC	TTCCCGCATG
8910	8920	8930	8940	8950	8960	8970	8980	8990	9000
ATCTTGACAT	TTCTGAAATA	AGCCCCCTTC	ACAATAATGA	TTGGGATCAA	ATTGCCAGAG	AAGAATCCAA	TCTTGCTGAA	CGACTTGGAG	TAGCTAAATC
9010	9020	9030	9040	9050	9060	9070	9080	9090	9100
TGAATTAAATT	AAACGTGTGC	CCGCATTAG	AGCAACTAGA	TGGCGTAGTC	ATGCAGCCGT	CCTTATATGG	CCTTCTTGTAA	TACCATTTCT	TGTTAAATC
9110	9120	9130	9140	9150	9160	9170	9180	9190	9200
CTACCTCATT	CTAACGTTCA	ACCAGTAGAA	CAATGGTACA	AGTTGATCAA	TGTTCATGT	AATACTATAT	CTGACTCAAT	TGATAGATGT	ATGGAGAATA
9210	9220	9230	9240	9250	9260	9270	9280	9290	9300
TTTCTATTAA	GCTTACTGGG	AAAAACAATC	TATTCTCTCG	ATCCAGAGGA	ACTGCAGGTG	CAGGTAAAAA	CAGTAAAATC	ACCCCTCAATG	ATATCCAATC
9310	9320	9330	9340	9350	9360	9370	9380	9390	9400
TATTTGGGAA	TCAAACAAATG	GGCAACCTAA	TGTATCTTTA	TGGCTTACAA	TTAAATACCA	AATGCGACAA	CTTATAATGC	ATCAAAGTTC	TCGTCAGCCG
9410	9420	9430	9440	9450	9460	9470	9480	9490	9500
ACTGATTAG	TTCACATTGT	TGACACACGA	TCTGGTCTAA	TAGTTATCAC	CCCTGAAGTT	GTTATTGTT	TTGATCGTT	AAATAGTGT	TTAATGTATT
9510	9520	9530	9540	9550	9560	9570	9580	9590	9600
TTACATTGAA	GATGACTTTA	ATGGTAAGTG	ACATGTTGAA	GGGAAGGATG	AATGTCACCG	CTCTCTGCAC	TATTAGTCAT	TACTTATCTC	CACTAGGGCC
9610	9620	9630	9640	9650	9660	9670	9680	9690	9700
AAGGATAGAT	AGATTGTTTT	CCATTGTAGA	TGAATTAGCA	CAACTATTAG	GTGACACTGT	ATATAAAGTT	ATTGCATCTC	TTGAATCTT	AGTATATGGG
9710	9720	9730	9740	9750	9760	9770	9780	9790	9800
TGTCTACAAC	TTAAAGATCC	AGTAGTGGAA	TTAGCAGGGT	CATTTCAATC	CTTTATTACA	CAAGAGAGTA	TAGATATCCT	AATTGGTCA	AAAGCCCTT
9810	9820	9830	9840	9850	9860	9870	9880	9890	9900
ATAAGGATGA	ATCAATAACT	GTACTACAC	AATTGTTAGA	TATATTTCTC	AACCTTTCTC	CAGATTTAAT	TGCTGAGATG	TTGTGCTCA	TGAGACTTTG
9910	9920	9930	9940	9950	9960	9970	9980	9990	10000
GGGTCATCCC	ACTCTTACTG	CTGCGCAAGC	TGCAGGTAAA	TGTGAGAGAAT	CTATGTGTG	AGGTAAGTTA	CTTGATTCTC	CTACAATAAT	GAAACTCTT
10010	10020	10030	10040	10050	10060	10070	10080	10090	10100
GCTTTTTCC	ACACAATTTC	AATTAATGGT	TACCGTAGAA	AGAAAAATGG	AATGTGGCCT	CCACTTATAC	TTCCCTAAAAA	TGCATCAAAA	AGCTTAATAG
10110	10120	10130	10140	10150	10160	10170	10180	10190	10200
AATTCAACA	TGATAATGCT	GAATATCTT	ACGAATATAC	ACTCAAGCAT	TGAAAGAGA	TCTCTCTCAT	AGAATTAGA	AAGTGCTTTG	ACTTTGATCC
10210	10220	10230	10240	10250	10260	10270	10280	10290	10300
TGGTGGGAG	CTAACGCATT	TATGAAAGA	CAAGGCAATA	AGTGCTCCAA	GAAGTGTGATG	GATGAGTGT	TTTCGTAGAA	GTCTAATAAA	ACAACGACAT
10310	10320	10330	10340	10350	10360	10370	10380	10390	10400
CAGAGACATC	ATATTCTAT	GCCCAATCCA	TTAAATAGAC	GTCTATTACT	CAATTCTTAA	GAAGATGACA	GTTTGATC	AGTTGCCGAG	CTTCAATATG
10410	10420	10430	10440	10450	10460	10470	10480	10490	10500
TTACCACTGG	TGAATATCTC	CAAGATGACA	CATTTGTGC	ATCTTACTCA	TTAAAGAGA	AAGAAATAAA	ACCAGATGGA	AGGATATTTG	CTAACGTTAC
10510	10520	10530	10540	10550	10560	10570	10580	10590	10600
TAATAGAATG	CGGTCTCTG	AACTAATTGC	GGAAGCAATT	CTCGCAAATC	ATGCAGGTAC	TCTAATGAAG	GAAAACGGAG	TTGTCTTGAA	TCAATTATCA
10610	10620	10630	10640	10650	10660	10670	10680	10690	10700
CTGACTAAAT	CATTGCTTAC	TATGAGTCAA	ATTGGCATAA	TATCAGAAAA	GGCGAAGAGA	TATACGCGAG	ATAACATCTC	ATCCCAAGGT	TTCCATACAA
10710	10720	10730	10740	10750	10760	10770	10780	10790	10800
TCAAGACTGA	TTCTAAAAAT	AAGAGGAAAAA	GCAAAACTGC	ATCATCATAC	CTCAGAGATC	CTGATGATAC	ATTGAACTT	AGTGCATGTT	TTATAACTAC
10810	10820	10830	10840	10850	10860	10870	10880	10890	10900
TGATCTTGCT	AAATACTGTC	TTCAATGGAG	ATATCAGACC	ATAATCCATT	TTGCTCGAAC	ATTAAACAGA	ATGTTATGGAG	TTCCACATTT	ATTGGAATGG
10910	10920	10930	10940	10950	10960	10970	10980	10990	11000
ATTATCTTC	GTTAAATTAG	ATCTACATTA	TATGTTGGTG	ATCCATTCAA	TCCTCTGCC	GCAACTGATG	CTTCGATCT	AGATAAAAGTA	TTAAATGGT
11010	11020	11030	11040	11050	11060	11070	11080	11090	11100
ATATCTTAT	AGTCTCTCCC	AAGGGAGGT	TTGAAGGCC	ATGTCAGAA	ATGTGGACAA	TGATCTCTAT	TTCTGTGATC	ATCCCTCTTT	CAGCCGAATC
11110	11120	11130	11140	11150	11160	11170	11180	11190	11200
CAAAACAAAGA	GTAATGAGCA	TGGTTCAAGG	AGATAATCAG	GCGATTGCGAG	TTACAACAAAG	AGTTCCCTAGA	TCATTACCTA	GTATTACGAA	AAAGGAGTTA
11210	11220	11230	11240	11250	11260	11270	11280	11290	11300
GCCTATGAG	CAAGCAAGT	ATTTTTGAA	AGACTTGGG	CAAATAATTA	TGGGTGGGT	CATCAGCTAA	AGGCTCAAGA	AACTATAATA	AGTTCCACGT
11310	11320	11330	11340	11350	11360	11370	11380	11390	11400
TCTTCATATA	TAGTAAACGG	GTATTTTATC	AAAGGACCTAT	ACTAACACAG	GCACTCAAAA	ATGCTAGCAA	GTTATGTC	ACTGCAGATG	TATTAGGTGA
11410	11420	11430	11440	11450	11460	11470	11480	11490	11500
ATGTAACCAA	GCTTCTGTT	CAAATTCTGC	TACTACCATC	ATGAGATTA	CAGAAAATGG	GGTTGAGAAA	GATAATGTT	ATAAGCTTAA	TATTTATCAG
11510	11520	11530	11540	11550	11560	11570	11580	11590	11600
TCCATTGTC	AACTCACATA	TGATCTAA	TTTCCCCAAT	ACTCCATACC	AGGTGAAACT	ATAAGTGA	TTTCTTAC	GCATCCAAGA	CTAACCTCAC

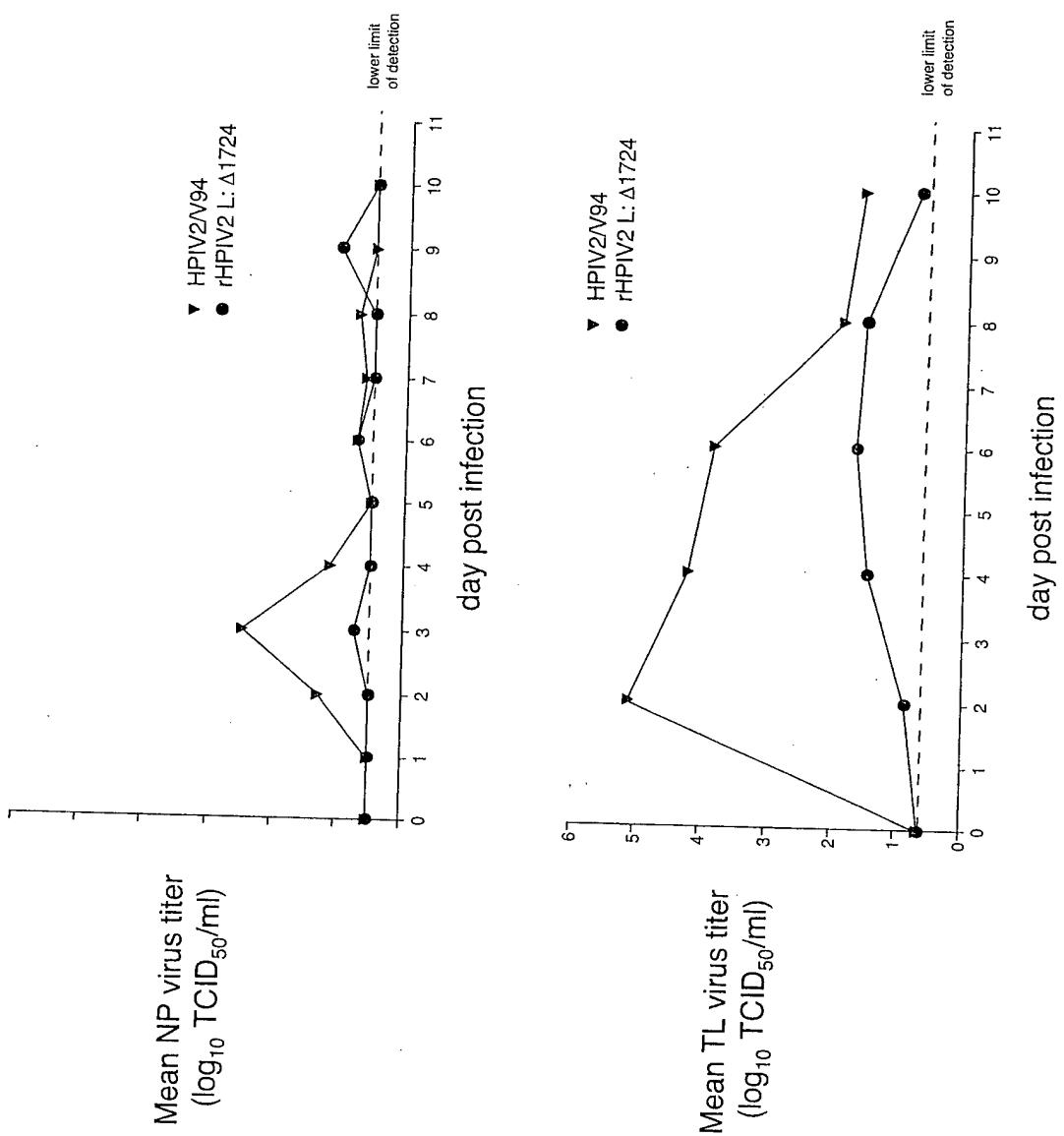
FIGURE 11D

11610	11620	11630	11640	11650	11660	11670	11680	11690	11700
GTATTGTTCT	GCTCCCTTC	CAGCTAGGTG	GTCTTAAATTA	CCTCGCATGT	AGCAGATTAT	TTAACCGCAA	TATCGGAGAT	CCTCTGGTA	CAGCTGTGGC
11710	11720	11730	11740	11750	11760	11770	11780	11790	11800
AGATCTCAAG	AGGTTAATTA	AATGTGGTGC	TCTTGAATCA	TGGATACTGT	ATAATTACT	AGCAAGAAA	CCAGGAAAG	GTTCATGGC	AACTTTAGCA
11810	11820	11830	11840	11850	11860	11870	11880	11890	11900
GCCGATCCAT	ACTCATTGAA	TCAAGAATAT	CTTTATCCTC	CTACTACTAT	ACTTAAAGA	CATACTCAA	ATACCTTAAT	GGAGATATGT	CGGAATCCCA
11910	11920	11930	11940	11950	11960	11970	11980	11990	12000
TGTTAAAGGG	AGTTTTACA	GATAATGCA	AAGAGGAGGA	AAATCTCC	GCAAAATTC	TTCTTGATCG	TGATATAGTA	TTGCCAAGAG	TTGCACACAT
12010	12020	12030	12040	12050	12060	12070	12080	12090	12100
TATAATAGAT	CAATCTAGCA	TCGGAAGGAA	GAACAGATA	CAAGGATTTC	TTGACACCAC	AAGGACCATA	ATGAGACGAT	CATTGAAAT	CAAACCACTC
12110	12120	12130	12140	12150	12160	12170	12180	12190	12200
TCAACTAAGA	AGACTCTTC	AGTCATAGAA	TATAATACTA	ATTACCTATC	TTATAACTAC	CCTGTACATC	TTAATCCTT	ACCTATTCC	GGATATTAA
12210	12220	12230	12240	12250	12260	12270	12280	12290	12300
ATTATATTAC	TGACCAAAC	TGCACTATTG	ATATATCTAG	AAAGTTAAGA	AAATTATCAT	GGTCTTCTT	ATTGAATGGA	AGAACCTTAG	AAGGATTAGA
12310	12320	12330	12340	12350	12360	12370	12380	12390	12400
AACTCCAGAT	CCAATTGAAAG	TTGTCAATGG	TTCTTGATT	GTAGGTACAG	GAGATTGTGA	TTTTGTATG	CAGGGTGACG	ACAAATTAC	TTGGTTCTT
12410	12420	12430	12440	12450	12460	12470	12480	12490	12500
TTACCTATGG	GGATAATTAT	TGATGGAAAT	CCTGAAACTA	ATCCACCCAT	CAGAGTCCA	TACATTGGGT	CTAGAACAGA	GGAAAGAAGA	GTTGCATCAA
12510	12520	12530	12540	12550	12560	12570	12580	12590	12600
TGGCATATAT	TAAAGGTGCC	ACACACAGTT	TGAAGGCTGC	TCTTAGAGGC	GCAGGGGTAT	ATATTGGGC	ATTGGGGAT	ACTGTACTGA	ACTGGAAATGA
12610	12620	12630	12640	12650	12660	12670	12680	12690	12700
TGCACCTGAT	ATCGCAAATA	CTAGGGTTAA	GATATCCCTA	GAGCAACTTC	AGACCCCTAC	ACCTCTTCCT	ACATCTGCAA	ACATTACACA	CCGTTAGAT
12710	12720	12730	12740	12750	12760	12770	12780	12790	12800
GATGGAGCCA	CAACACTTAA	ATTCACTCCA	GCTAGTCCCT	ATGCATTTTC	TAGTTTACT	CATATATCAA	ATGATCAACA	ATATTTAGAA	ATAGATCAGA
12810	12820	12830	12840	12850	12860	12870	12880	12890	12900
GAGTAGTCGA	TTCTAATATT	ATTATCAAC	AATTAATGAT	AAACAGGACTT	GGGATTATTG	AGACCTACCA	TAACCCACCT	ATAAGGACTT	CTACACAAAGA
12910	12920	12930	12940	12950	12960	12970	12980	12990	13000
AATCACTCTC	CATTGACACA	CTAGCTCATC	TTGTTGTGTT	AGAAGGTGAG	ATGGTTGCCT	TATATGTGAG	AGCAATGGAG	AGGTTCTCA	GATCACTGTT
13010	13020	13030	13040	13050	13060	13070	13080	13090	13100
CCCTACTA	ATACATTGTC	ATATGATCCT	GATCCACTAG	CAGATTATGA	GATTGCACAC	CTAGATTATC	TCTCCTACCA	AGCTAAAATT	GGAAGTACAG
13110	13120	13130	13140	13150	13160	13170	13180	13190	13200
ATTACTACTC	ACTCACTGAT	AAAATTGAC	TATTAGCACA	TTAAACTGCA	AAACAAATGA	TAACACTCAAT	AATTGGGTTA	GATGAAACAG	TATCAATTG
13210	13220	13230	13240	13250	13260	13270	13280	13290	13300
CAATGATGCG	GTTATCCTAT	CTGACTATAC	TAATAACTGG	ATTAGTGAAT	GTTCTTATAC	TAAGATAGAT	TTAGTTTTA	AATTAATGGC	ATGGAATTTC
13310	13320	13330	13340	13350	13360	13370	13380	13390	13400
CTTCTTGAGC	TTGCATTC	GATGACTAC	TAAAGGATAT	CATCTGGAC	AAATATATT	GACTATAC	ATATGACTTT	ACGCAGGATA	CCCGGAAC
13410	13420	13430	13440	13450	13460	13470	13480	13490	13500
CTCTAAATAA	TATTGAGCT	ACTATTAGCC	ATCCAAAATT	ATTAAGACG	GCAATGAATC	TTGATATTAT	CACTCCTATA	CATGCACCGT	ATTTAGCTTC
13510	13520	13530	13540	13550	13560	13570	13580	13590	13600
ATTAGATTAT	GTCAAATTA	GTATTGATGC	AATTCACTG	GGAGTTAAC	AAAGTCTG	TGATTATCA	AATGGAATTG	ATCTTGAAAT	CTTGATTCTT
13610	13620	13630	13640	13650	13660	13670	13680	13690	13700
TCAGAGGATT	CAATGGAAAT	TAGTGATAGG	GCAATGAATC	TCATTGCTAG	AAAACAACT	CTCCTTGAC	TTGTTAAAGG	TGAGAACTAT	ACTTTCCAA
13710	13720	13730	13740	13750	13760	13770	13780	13790	13800
AAATTAAAGG	GATGCCACCA	GAAGAAAAGT	GTTCAGTCTT	AACGAATAT	CTAGCAATG	GTTATCAAA	TACTCATCAC	TTAGATCCAG	ATCTTCAAA
13810	13820	13830	13840	13850	13860	13870	13880	13890	13900
GTATTTATAT	AATCTAACTA	ATCCAAAATT	GACTGCATT	CCCAGTAACA	ACTTCTACTT	AACTAGAAA	ATCCTTAATC	AAATTAGAGA	ATCAGACGAA
13910	13920	13930	13940	13950	13960	13970	13980	13990	14000
GGACAATATA	TTATCACCTC	ATATTATGAA	TCCTTCGAA	AATTAGAAAC	AGATATAATT	CTTCACTCTA	CTTAACTGTC	TCCTTATGAT	AATTCAAGAA
14010	14020	14030	14040	14050	14060	14070	14080	14090	14100
CTCTAACAAA	GTTGATTTA	TCCCTTGAC	TCTTCCAC	TCCAGAAATCT	CTCGAGAAAT	ATCCCTCTTC	AGTTGTATC	GACTCTCGAT	CTGCAATTTC
14110	14120	14130	14140	14150	14160	14170	14180	14190	14200
AAACACTAATT	CCAGGCCCTC	CTTCTCATCA	TGTATTACGA	CCACTAGGAG	TGTCATCCAC	AGCTGGTAT	AAAGGGATAA	GTTATTGTAG	ATACCTAGAA
14210	14220	14230	14240	14250	14260	14270	14280	14290	14300
ACACAAAAAGA	TACAGACTGG	TGATCATCTT	TATTTAGCCG	AAGGAAGCGG	TGCTTCAATG	TCACTTCTAG	AACTCTTATT	TCCAGGAGAT	ACTGTCTATT
14310	14320	14330	14340	14350	14360	14370	14380	14390	14400
ATAATAGTCT	TTTTAGTAGT	GGAGAGAAATC	CTCCACAGAG	AAACTATGCC	CCTCTTCCAA	CTCAATTGTT	ACAGAGTGTG	CCATATAAAT	TGTGGCAAGC
14410	14420	14430	14440	14450	14460	14470	14480	14490	14500
TGATCTTGCT	GATGATAGCA	ATTGATAA	AGATTTGTC	CCATTATGGA	ATGGAAACGG	TGCAAGTTACA	GAACCTATCAA	CAAAGGATGC	AGTTGCATTC

FIGURE 11E

14510	14520	14530	14540	14550	14560	14570	14580	14590	14600
ATAATACATA	AAGTAGGAGC	AGAGAAAGCA	TCCCTTGTC	ATATAGATCT	CGAATCAACT	GCTAATATAA	ATCAGCAAAC	TCTGTCCAGA	TCCCAGATTC
14610	14620	14630	14640	14650	14660	14670	14680	14690	14700
ATTCATTAAT	TATAGCAACT	ACTGTTCTTA	AGAGGGGTGG	GATATTAAATT	TATAAAACAT	CATGGCTTC	GTTTCTAGG	TTTAGTCAC	TAGCAAGTCT
14710	14720	14730	14740	14750	14760	14770	14780	14790	14800
ACTTTGGTGC	TTCTTGACC	GGATCCATCT	AATACGTTAGT	AGCTATTCTG	ATCCTCACAG	TCATGAGGTT	TATCTTGTAT	GTAGACTTGC	CGCAGATTTC
14810	14820	14830	14840	14850	14860	14870	14880	14890	14900
AGAACTATCG	GTTCAGTGC	AGCTCTAGTA	ACTGCTACTA	CTCTTCACAA	TGACGGATTTC	ACAACAATAC	ATCCTGATGT	TGTTTGTAGT	TATTGGCAAC
14910	14920	14930	14940	14950	14960	14970	14980	14990	15000
ACCATCTTGA	AAATGTTGGG	AGAGTCGGAA	AGATAATTGA	TGAGATACTT	GATGGTTAG	CCACCAACTT	CTTCGCAGGA	GATAATGGGC	TTATTCTAACG
15010	15020	15030	15040	15050	15060	15070	15080	15090	15100
ATGTGGAGGA	ACTCCCGACT	CCAGAAAATG	GTTAGAGATT	GACCAGTTAG	CATCATTTGA	TTGGTTCAA	GATGCTCTGG	TTACACTTAT	CACTATACAC
15110	15120	15130	15140	15150	15160	15170	15180	15190	15200
CTAAAGGAAA	TTATAGAAAGT	GCAGTCATCA	CATACAGAGG	ATTATACATC	TCTCCTCTTC	ACACCTTATA	ATATTGGTGC	AGCAGGGAAA	GTCAGAACTA
15210	15220	15230	15240	15250	15260	15270	15280	15290	15300
TCATCAAATT	AATTCTAGAA	CGATCTTAA	TGTATACAGT	CCGAAATTGG	TTAGTTTAC	CCAGTTCCAT	CCGGGATTCT	GTACGACAAG	ATTTAGAAATT
15310	15320	15330	15340	15350	15360	15370	15380	15390	15400
AGGGTCATTT	AGATTAATGT	CTATTTTAAG	TGAACAGACA	TTTCTTAAAAA	AGACACCCAC	AAAAAAATAC	TTACTTGATC	AGCTTACAAG	GACATATATA
15410	15420	15430	15440	15450	15460	15470	15480	15490	15500
TCAACCTCT	TTAACTCTCA	CTCAGTCCTT	CCCCCTCCACC	GTCCCATATCA	AAAACAAATA	TGGAAAGCCT	TAGGTAGTGT	AATATATTGT	TCGGAGACAG
15510	15520	15530	15540	15550	15560	15570	15580	15590	15600
TTGATATACC	TCTAATTAAA	GACATTCAAGA	TAGAAGATAT	TAATGATTT	GAAGATATCG	AGAGGGTAT	CGATGGCGAA	GAATTATGAC	AAACATGATT
15610	15620	15630	15640	15650					
ATAAGAACTC	ATGATAGTTT	TATTTAAGAA	AAACATATTG	ATTTTCCCT	TGGT				

FIGURE 12



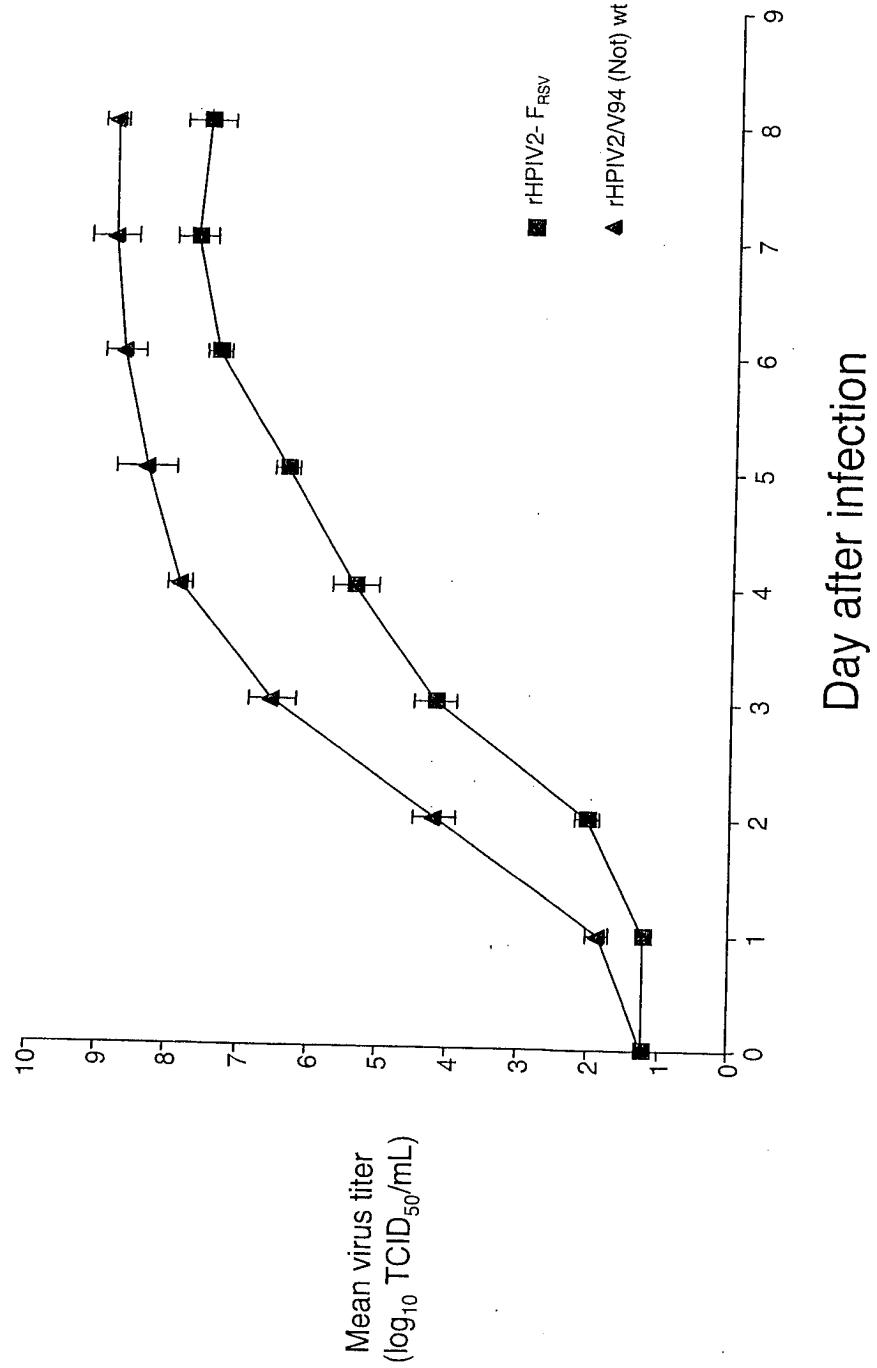


FIGURE 13

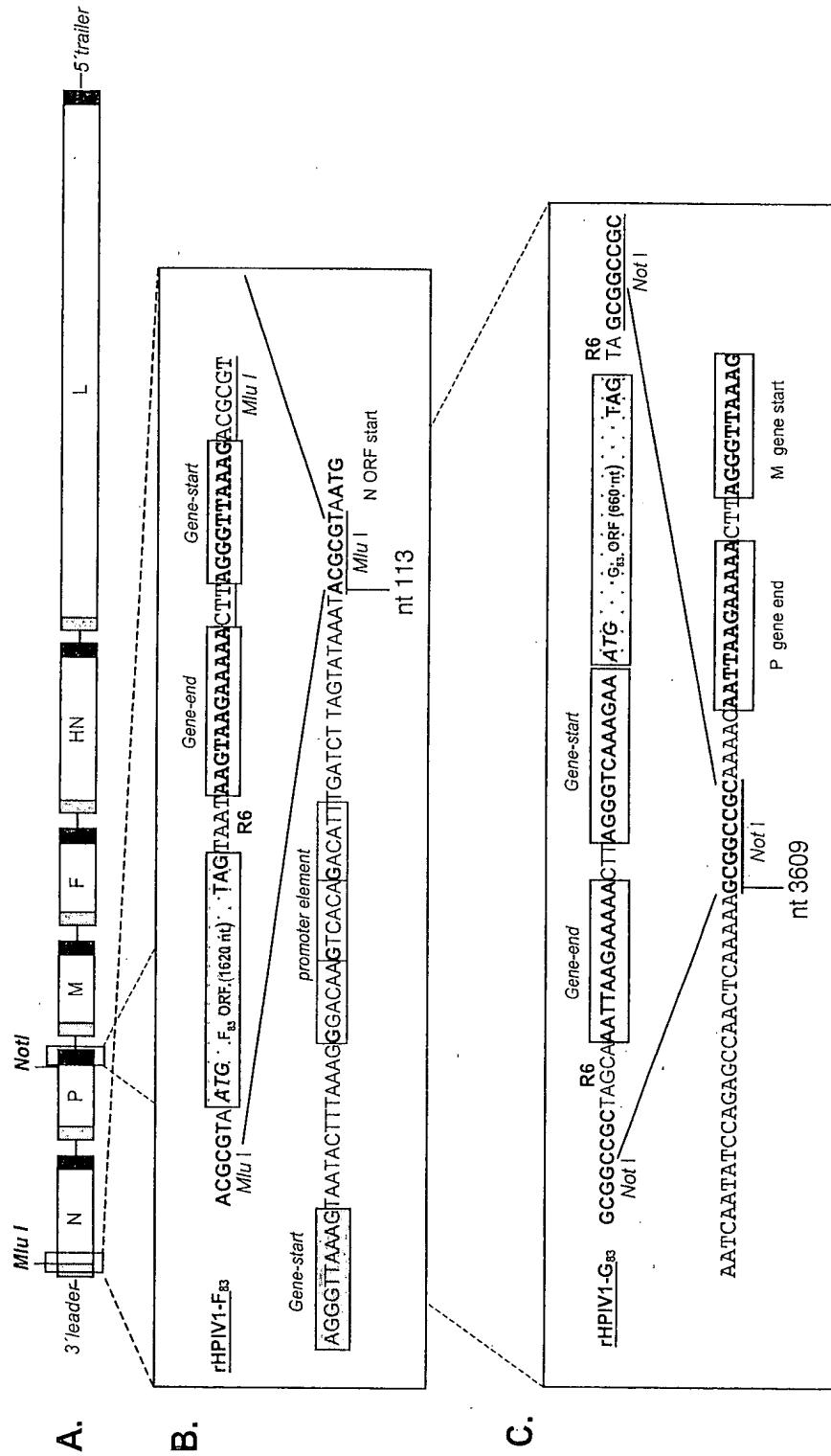


FIGURE 14